



PATENT
Docket No.: 22221/1030 (RU 339CIP)

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicants : O'Donnell et al.

Serial No. : 09/716,964

Cnfrm. No. : 2211

Filed : November 21, 2000

For : ENZYMES DERIVED FROM
THERMOPHILIC ORGANISMS THAT
FUNCTION AS A CHROMOSOMAL
REPLICASE, AND PREPARATION AND
USES THEREOF

Examiner:
R. Hutson

Art Unit:
1652

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STATEMENT IN ACCORDANCE WITH 37 C.F.R. § 1.821

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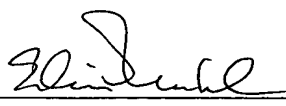
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Alexandria, VA 22313-1450

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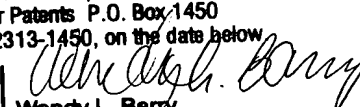
In accordance with 37 C.F.R. § 1.821, applicants hereby submit a Sequence Listing (167 pages) on paper and on a computer readable 3.5" Diskette. In accordance with 37 C.F.R. § 1.821(f), applicants submit that the contents of the paper copy and the computer readable form are the same. In accordance with 37 C.F.R. § 1.821(g), applicants submit that the Sequence Listing contains no new matter.

Respectfully submitted,

Dated: February 4, 2004


Edwin V. Merkel
Registration No. 40,087

NIXON PEABODY LLP
Clinton Square, P.O. Box 31051
Rochester, New York 14603-1051
Telephone: (585) 263-1128
Facsimile: (585) 263-1600

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I hereby certify that this correspondence is being deposited with the United States Postal Service as first class mail in an envelope addressed to: Commissioner for Patents P.O. Box 1450 Alexandria, VA 22313-1450, on the date below	
Date <u>2/4/04</u>	 Wendy L. Barry



SEQUENCE LISTING

<110> O'Donnell, Michael E.
Yurieva, Olga

<120> ENZYMES DERIVED FROM THERMOPHILIC ORGANISMS THAT
FUNCTION AS A CHROMOSOMAL REPLICASE, PREPARATION AND
USE THEREOF

<130> 22221/1030

<140> 09/716,964

<141> 2000-11-21

<150> 09/642,218

<151> 2000-08-18

<150> 09/057,416

<151> 1998-04-08

<150> 60/143,202

<151> 1997-04-08

<160> 212

<170> PatentIn Ver. 2.1

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<212> DNA

<213> Thermus thermophilus

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<211> 529

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<213> *Thermus thermophilus*

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35 40 45

Lys Thr Thr Thr Ala Arg Leu Leu Ala Met Ala Val Gly Cys Gln Gly
50 55 60

Glu Asp Pro Pro Cys Gly Val Cys Pro His Cys Gln Ala Val Gln Arg
65 70 75 80

Gly Ala His Pro Asp Val Val Asp Ile Asp Ala Ala Ser Asn Asn Ser
85 90 95

Val Glu Asp Val Arg Glu Leu Arg Glu Arg Ile His Leu Ala Pro Leu
100 105 110

Ser Ala Pro Arg Lys Val Phe Ile Leu Asp Glu Ala His Met Leu Ser
 115 120 125

Lys Ser Ala Phe Asn Ala Leu Leu Lys Thr Leu Glu Glu Pro Pro Pro
 130 135 140

His Val Leu Phe Val Phe Ala Thr Thr Glu Pro Glu Arg Met Pro Pro
 145 150 155 160

Thr Ile Leu Ser Arg Thr Gln His Phe Arg Phe Arg Arg Leu Thr Glu
 165 170 175

Glu Glu Ile Ala Phe Lys Leu Arg Arg Ile Leu Glu Ala Val Gly Arg
 180 185 190

Glu Ala Glu Glu Glu Ala Leu Leu Leu Leu Ala Arg Leu Ala Asp Gly
 195 200 205

Ala Leu Arg Asp Ala Glu Ser Leu Leu Glu Arg Phe Leu Leu Leu Glu
 210 215 220

Gly Pro Leu Thr Arg Lys Glu Val Glu Arg Ala Leu Gly Ser Pro Pro
 225 230 235 240

Gly Thr Gly Val Ala Glu Ile Ala Ala Ser Leu Ala Arg Gly Lys Thr
 245 250 255

Ala Glu Ala Leu Gly Leu Ala Arg Arg Leu Tyr Gly Glu Gly Tyr Ala
 260 265 270

Pro Arg Ser Leu Val Ser Gly Leu Leu Glu Val Phe Arg Glu Gly Leu
 275 280 285

Tyr Ala Ala Phe Gly Leu Ala Gly Thr Pro Leu Pro Ala Pro Pro Gln
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Ala Leu Ile Ala Ala Met Thr Ala Leu Asp Glu Ala Met Glu Arg Leu
 305 310 315 320

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 325 330 335

Gly Arg Ala Leu Ala Ala Glu Ala Leu Pro Gln Pro Thr Gly Ala Pro
 340 345 350

Ser Pro Glu Val Gly Pro Lys Pro Glu Ser Pro Pro Thr Pro Glu Pro
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 Pro Glu Val Arg Glu Gly Gln Leu Cys Leu Ala Phe Pro Glu Asp Lys
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 Glu Ala Ala Glu Glu Ala Pro Glu Glu Ala Leu Arg Arg Val Val Arg
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<211> 1590

<212> DNA

<213> *Thermus thermophilus*

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<213> *Thermus thermophilus*

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Lys Thr Thr Thr Ala Arg Leu Leu Ala Met Ala Val Gly Cys Gln Gly
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Glu Asp Pro Pro Cys Gly Val Cys Pro His Cys Gln Ala Val Gln Arg
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Gly Ala His Pro Asp Val Val Asp Ile Asp Ala Ala Ser Asn Asn Ser
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Lys Ser Ala Phe Asn Ala Leu Leu Lys Thr Leu Glu Glu Pro Pro Pro
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His Val Leu Phe Val Phe Ala Thr Thr Glu Pro Glu Arg Met Pro Pro
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Thr Ile Leu Ser Arg Thr Gln His Phe Arg Phe Arg Arg Leu Thr Glu
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Glu Glu Ile Ala Phe Lys Leu Arg Arg Ile Leu Glu Ala Val Gly Arg
 180 185 190

Glu Ala Glu Glu Glu Ala Leu Leu Leu Leu Ala Arg Leu Ala Asp Gly
 195 200 205

Ala Leu Arg Asp Ala Glu Ser Leu Leu Glu Arg Phe Leu Leu Leu Glu
 210 215 220

Gly Pro Leu Thr Arg Lys Glu Val Glu Arg Ala Leu Gly Ser Pro Pro
 225 230 235 240

Gly Thr Gly Val Ala Glu Ile Ala Ala Ser Leu Ala Arg Gly Lys Thr
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Ala Glu Ala Leu Gly Leu Ala Arg Arg Leu Tyr Gly Glu Gly Tyr Ala
 260 265 270

Pro Arg Ser Leu Val Ser Gly Leu Leu Glu Val Phe Arg Glu Gly Leu
 275 280 285

Tyr Ala Ala Phe Gly Leu Ala Gly Thr Pro Leu Pro Ala Pro Pro Gln
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Ala Leu Ile Ala Ala Met Thr Ala Leu Asp Glu Ala Met Glu Arg Leu
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Ala Arg Arg Ser Asp Ala Leu Ser Leu Glu Val Ala Leu Leu Glu Ala
 325 330 335

Gly Arg Ala Leu Ala Ala Glu Ala Leu Pro Gln Pro Thr Gly Ala Pro
 340 345 350

Ser Pro Glu Val Gly Pro Lys Pro Glu Ser Pro Pro Thr Pro Glu Pro
 355 360 365

Pro Arg Pro Glu Glu Ala Pro Asp Leu Arg Glu Arg Trp Arg Ala Phe
 370 375 380
 Leu Glu Ala Leu Arg Pro Thr Leu Arg Ala Phe Val Arg Glu Ala Arg
 385 390 395 400
 Pro Glu Val Arg Glu Gly Gln Leu Cys Leu Ala Phe Pro Glu Asp Lys
 405 410 415
 Ala Phe His Tyr Arg Lys Ala Ser Glu Gln Lys Val Arg Leu Leu Pro
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<210> 5
 <211> 454
 <212> PRT
 <213> *Thermus thermophilus*

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 35 40 45
 Lys Thr Thr Thr Ala Arg Leu Leu Ala Met Ala Val Gly Cys Gln Gly
 50 55 60
 Glu Asp Pro Pro Cys Gly Val Cys Pro His Cys Gln Ala Val Gln Arg
 65 70 75 80
 Gly Ala His Pro Asp Val Val Asp Ile Asp Ala Ala Ser Asn Asn Ser
 85 90 95
 Val Glu Asp Val Arg Glu Leu Arg Glu Arg Ile His Leu Ala Pro Leu
 100 105 110

Ser Ala Pro Arg Lys Val Phe Ile Leu Asp Glu Ala His Met Leu Ser
 115 120 125

Lys Ser Ala Phe Asn Ala Leu Leu Lys Thr Leu Glu Glu Pro Pro Pro
 130 135 140

His Val Leu Phe Val Phe Ala Thr Thr Glu Pro Glu Arg Met Pro Pro
 145 150 155 160

Thr Ile Leu Ser Arg Thr Gln His Phe Arg Phe Arg Arg Leu Thr Glu
 165 170 175

Glu Glu Ile Ala Phe Lys Leu Arg Arg Ile Leu Glu Ala Val Gly Arg
 180 185 190

Glu Ala Glu Glu Glu Ala Leu Leu Leu Leu Ala Arg Leu Ala Asp Gly
 195 200 205

Ala Leu Arg Asp Ala Glu Ser Leu Leu Glu Arg Phe Leu Leu Leu Glu
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Gly Pro Leu Thr Arg Lys Glu Val Glu Arg Ala Leu Gly Ser Pro Pro
 225 230 235 240

Gly Thr Gly Val Ala Glu Ile Ala Ala Ser Leu Ala Arg Gly Lys Thr
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Ala Glu Ala Leu Gly Leu Ala Arg Arg Leu Tyr Gly Glu Gly Tyr Ala
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Pro Arg Ser Leu Val Ser Gly Leu Leu Glu Val Phe Arg Glu Gly Leu
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Tyr Ala Ala Phe Gly Leu Ala Gly Thr Pro Leu Pro Ala Pro Pro Gln
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Ala Leu Ile Ala Ala Met Thr Ala Leu Asp Glu Ala Met Glu Arg Leu
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Ala Arg Arg Ser Asp Ala Leu Ser Leu Glu Val Ala Leu Leu Glu Ala
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Gly Arg Ala Leu Ala Ala Glu Ala Leu Pro Gln Pro Thr Gly Ala Pro
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Ser Pro Glu Val Gly Pro Lys Pro Glu Ser Pro Pro Thr Pro Glu Pro
 355 360 365

Pro Arg Pro Glu Glu Ala Pro Asp Leu Arg Glu Arg Trp Arg Ala Phe
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Leu Glu Ala Leu Arg Pro Thr Leu Arg Ala Phe Val Arg Glu Ala Arg
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Pro Glu Val Arg Glu Gly Gln Leu Cys Leu Ala Phe Pro Glu Asp Lys
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Ala Phe His Tyr Arg Lys Ala Ser Glu Gln Lys Val Arg Leu Leu Pro
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Gly Glu Lys Lys Lys Ala
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<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

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<210> 7

<211> 8

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: peptide

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<210> 8

<211> 34

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: primer

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<210> 9

<211> 9

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: peptide

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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: primer

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<212> DNA

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<223> Description of Artificial Sequence: primer

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<213> Artificial Sequence

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<223> Description of Artificial Sequence: peptide

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<221> PEPTIDE

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<211> 12

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: peptide

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<210> 19

<211> 180

<212> PRT

<213> Escherichia coli

<400> 19

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Ser Leu Gly Arg Ile His His Ala Tyr Leu Phe Ser Gly Thr Arg Gly
35 40 45

Val Gly Lys Thr Ser Ile Ala Arg Leu Leu Ala Lys Gly Leu Asn Cys
50 55 60

Glu Thr Gly Ile Thr Ala Thr Pro Cys Gly Val Cys Asp Asn Cys Arg
65 70 75 80

Glu Ile Glu Gln Gly Arg Phe Val Asp Leu Ile Glu Ile Asp Ala Ala
85 90 95

Ser Arg Thr Lys Val Glu Asp Thr Arg Asp Leu Leu Asp Asn Val Gln
100 105 110

Tyr Ala Pro Ala Arg Gly Arg Phe Lys Val Tyr Leu Ile Asp Glu Val
115 120 125

His Met Leu Ser Arg His Ser Phe Asn Ala Leu Leu Lys Thr Leu Glu
130 135 140

Glu Pro Pro Glu His Val Lys Phe Leu Leu Ala Thr Thr Asp Pro Gln
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Lys Leu Pro Val Thr Ile Leu Ser Arg Cys Leu Gln Phe His Leu Lys
165 170 175

Ala Leu Asp Val
180

<210> 20

<211> 180

<212> PRT

<213> *Bacillus subtilis*

<400> 20

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Leu Gln Lys Lys Phe Ser His Ala Tyr Leu Phe Ser Gly Pro Arg Gly
35 40 45

Thr Gly Lys Thr Ser Ala Ala Lys Ile Phe Ala Lys Ala Val Asn Cys
50 55 60

Glu His Ala Pro Val Asp Glu Pro Cys Asn Glu Cys Ala Ala Cys Lys
65 70 75 80

Gly Ile Thr Asn Gly Ser Ile Ser Asp Val Ile Glu Ile Asp Ala Ala
85 90 95

Ser Asn Asn Gly Val Asp Glu Ile Arg Asp Ile Arg Asp Lys Val Lys
100 105 110

Phe Ala Pro Ser Ala Val Thr Tyr Lys Val Tyr Ile Ile Asp Glu Val
115 120 125

His Met Leu Ser Ile Gly Ala Phe Asn Ala Leu Leu Lys Thr Leu Glu
130 135 140

Glu Pro Pro Glu His Cys Ile Phe Ile Leu Ala Thr Thr Glu Pro His
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Lys Ile Pro Leu Thr Ile Ile Ser Arg Cys Gln Arg Phe Asp Phe Lys
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Arg Ile Thr Ser
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<210> 21

<211> 294

<212> PRT

<213> *Escherichia coli*

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Ser Leu Gly Arg Ile His His Ala Tyr Leu Phe Ser Gly Thr Arg Gly	35	40	45
Val Gly Lys Thr Ser Ile Ala Arg Leu Leu Ala Lys Gly Leu Asn Cys	50	55	60
Glu Thr Gly Ile Thr Ala Thr Pro Cys Gly Val Cys Asp Asn Cys Arg	65	70	75
Glu Ile Glu Gln Gly Arg Phe Val Asp Leu Ile Glu Ile Asp Ala Ala	85	90	95
Ser Arg Thr Lys Val Glu Asp Thr Arg Asp Leu Leu Asp Asn Val Gln	100	105	110
Tyr Ala Pro Ala Arg Gly Arg Phe Lys Val Tyr Leu Ile Asp Glu Val	115	120	125
His Met Leu Ser Arg His Ser Phe Asn Ala Leu Leu Lys Thr Leu Glu	130	135	140
Glu Pro Pro Glu His Val Lys Phe Leu Leu Ala Thr Thr Asp Pro Gln	145	150	155
Lys Leu Pro Val Thr Ile Leu Ser Arg Cys Leu Gln Phe His Leu Lys	165	170	175
Ala Leu Asp Val Glu Gln Ile Arg His Gln Leu Glu His Ile Leu Asn	180	185	190
Glu Glu His Ile Ala His Glu Pro Arg Ala Leu Gln Leu Leu Ala Arg	195	200	205
Ala Ala Glu Gly Ser Leu Arg Asp Ala Leu Ser Leu Thr Asp Gln Ala	210	215	220
Ile Ala Ser Gly Asp Gly Gln Val Ser Thr Gln Ala Val Ser Ala Met	225	230	235
Leu Gly Thr Leu Asp Asp Asp Gln Ala Leu Ser Leu Val Glu Ala Met	245	250	255
Val Glu Ala Asn Gly Glu Arg Val Met Ala Leu Ile Asn Glu Ala Ala			

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Val Gly Lys Thr Ser Ile Ala Arg Leu Phe Ala Lys Gly Leu Asn Cys		
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Val His Gly Val Thr Ala Thr Pro Cys Gly Glu Cys Glu Asn Cys Lys		
65	70	75 80
Ala Ile Glu Gln Gly Asn Phe Ile Asp Leu Ile Glu Ile Asp Ala Ala		
85	90	95
Ser Arg Thr Lys Val Glu Asp Thr Arg Glu Leu Leu Asp Asn Val Gln		
100	105	110
Tyr Lys Pro Val Val Gly Arg Phe Lys Val Tyr Leu Ile Asp Glu Val		
115	120	125
His Met Leu Ser Arg His Ser Phe Asn Ala Leu Leu Lys Thr Leu Glu		
130	135	140
Glu Pro Pro Glu Tyr Val Lys Phe Leu Leu Ala Thr Thr Asp Pro Gln		
145	150	155 160
Lys Leu Pro Val Thr Ile Leu Ser Arg Cys Leu Gln Phe His Leu Lys		
165	170	175

Ala Leu Asp Glu Thr Gln Ile Ser Gln His Leu Ala His Ile Leu Thr
180 185 190

Gln Glu Asn Ile Pro Phe Glu Asp Pro Ala Leu Val Lys Leu Ala Lys
195 200 205

Ala Ala Gln Gly Ser Ile Arg Asp Ser Leu Ser Leu Thr Asp Gln Ala
210 215 220

Ile Ala Met Gly Asp Arg Gln Val Thr Asn Asn Val Val Ser Asn Met
225 230 235 240

Leu Gly Leu Leu Asp Asp Asn Tyr Ser Val Asp Ile Leu Tyr Ala Leu
245 250 255

His Gln Gly Asn Gly Glu Leu Leu Met Arg Thr Leu Gln Arg Val Ala
260 265 270

Asp Ala Ala Gly Asp Trp Asp Lys Leu Leu Gly Glu Cys Ala Glu Lys
275 280 285

Leu His Gln Ile Ala Leu
290

<210> 23

<211> 294

<212> PRT

<213> Bacillus subtilis

<400> 23

Met Ser Tyr Gln Ala Leu Tyr Arg Val Phe Arg Pro Gln Arg Phe Glu
1 5 10 15

Asp Val Val Gly Gln Glu His Ile Thr Lys Thr Leu Gln Asn Ala Leu
20 25 30

Leu Gln Lys Lys Phe Ser His Ala Tyr Leu Phe Ser Gly Pro Arg Gly
35 40 45

Thr Gly Lys Thr Ser Ala Ala Lys Ile Phe Ala Lys Ala Val Asn Cys
50 55 60

Glu His Ala Pro Val Asp Glu Pro Cys Asn Glu Cys Ala Ala Cys Lys
65 70 75 80

Gly Ile Thr Asn Gly Ser Ile Ser Asp Val Ile Glu Ile Asp Ala Ala
85 90 95

Ser Asn Asn Gly Val Asp Glu Ile Arg Asp Ile Arg Asp Lys Val Lys
100 105 110

Phe Ala Pro Ser Ala Val Thr Tyr Lys Val Tyr Ile Ile Asp Glu Val
115 120 125

His Met Leu Ser Ile Gly Ala Phe Asn Ala Leu Leu Lys Thr Leu Glu
130 135 140

Glu Pro Pro Glu His Cys Ile Phe Ile Leu Ala Thr Thr Glu Pro His
145 150 155 160

Lys Ile Pro Leu Thr Ile Ile Ser Arg Cys Gln Arg Phe Asp Phe Lys
165 170 175

Arg Ile Thr Ser Gln Ala Ile Val Gly Arg Met Asn Lys Ile Val Asp
180 185 190

Ala Glu Gln Leu Gln Val Glu Glu Gly Ser Leu Glu Ile Ile Ala Ser
195 200 205

Ala Ala His Gly Gly Met Arg Asp Ala Leu Ser Leu Leu Asp Gln Ala
210 215 220

Ile Ser Phe Ser Gly Asp Ile Leu Lys Val Glu Asp Ala Leu Leu Ile
225 230 235 240

Thr Gly Ala Val Ser Gln Leu Tyr Ile Gly Lys Leu Ala Lys Ser Leu
245 250 255

His Asp Lys Asn Val Ser Asp Ala Leu Glu Thr Leu Asn Glu Leu Leu
260 265 270

Gln Gln Gly Lys Asp Pro Ala Lys Leu Ile Glu Asp Met Ile Phe Tyr
275 280 285

Phe Arg Asp Met Leu Leu
290

<210> 24

<211> 300

<212> PRT

<213> *Caulobacter crescentus*

<400> 24

Asp Ala Tyr Thr Val Leu Ala Arg Lys Tyr Arg Pro Arg Thr Phe Glu

1	5	10	15
Asp Leu Ile Gly Gln Glu Ala Met Val Arg Thr Leu Ala Asn Ala Phe	20	25	30
Ser Thr Gly Arg Ile Ala His Ala Phe Met Leu Thr Gly Val Arg Gly	35	40	45
Val Gly Lys Thr Thr Thr Ala Arg Leu Leu Ala Arg Ala Leu Asn Tyr	50	55	60
Glu Thr Asp Thr Val Lys Gly Pro Ser Val Asp Leu Thr Thr Glu Gly	65	70	75
Tyr His Cys Arg Ser Ile Ile Glu Gly Arg His Met Asp Val Leu Glu	85	90	95
Leu Asp Ala Ala Ser Arg Thr Lys Val Asp Glu Met Arg Glu Leu Leu	100	105	110
Asp Gly Val Arg Tyr Ala Pro Val Glu Ala Arg Tyr Lys Val Tyr Ile	115	120	125
Ile Asp Glu Val His Met Leu Ser Thr Ala Ala Phe Asn Ala Leu Leu	130	135	140
Lys Thr Leu Glu Glu Pro Pro Pro His Ala Lys Phe Ile Phe Ala Thr	145	150	155
Thr Glu Ile Arg Lys Val Pro Val Thr Ile Leu Ser Arg Cys Gln Arg	165	170	175
Phe Asp Leu Arg Arg Val Glu Pro Asp Val Leu Val Lys His Phe Asp	180	185	190
Arg Ile Ser Ala Lys Glu Gly Ala Arg Ile Glu Met Asp Ala Leu Ala	195	200	205
Leu Ile Ala Arg Ala Ala Glu Gly Ser Val Arg Asp Gly Leu Ser Leu	210	215	220
Leu Asp Gln Ala Ile Val Gln Thr Glu Arg Gly Gln Thr Val Thr Ser	225	230	235
Thr Val Val Arg Asp Met Leu Gly Leu Ala Asp Arg Ser Gln Thr Ile	245	250	255
Ala Leu Tyr Glu His Val Met Ala Gly Lys Thr Lys Asp Ala Leu Glu			

260	265	270
Gly Phe Arg Ala Leu Trp Gly Phe Gly Ala Asp Pro Ala Val Val Met		
275	280	285
Leu Asp Val Leu Asp His Cys His Ala Ser Ala Val		
290	295	300
<210> 25		
<211> 260		
<212> PRT		
<213> Mycoplasma genitalium		
<400> 25		
Met His Gln Val Phe Tyr Gln Lys Tyr Arg Pro Ile Asn Phe Lys Gln		
1	5	10 15
Thr Leu Gly Gln Glu Ser Ile Arg Lys Ile Leu Val Asn Ala Ile Asn		
20	25	30
Arg Asp Lys Leu Pro Asn Gly Tyr Ile Phe Ser Gly Glu Arg Gly Thr		
35	40	45
Gly Lys Thr Thr Phe Ala Lys Ile Ile Ala Lys Ala Ile Asn Cys Leu		
50	55	60
Asn Trp Asp Gln Ile Asp Val Cys Asn Ser Cys Asp Val Cys Lys Ser		
65	70	75 80
Ile Asn Thr Asn Ser Ala Ile Asp Ile Val Glu Ile Asp Ala Ala Ser		
85	90	95
Lys Asn Gly Ile Asn Asp Ile Arg Glu Leu Val Glu Asn Val Phe Asn		
100	105	110
His Pro Phe Thr Phe Lys Lys Lys Val Tyr Ile Leu Asp Glu Ala His		
115	120	125
Met Leu Thr Thr Gln Ser Trp Gly Gly Leu Leu Lys Thr Leu Glu Glu		
130	135	140
Ser Pro Pro Tyr Val Leu Phe Ile Phe Thr Thr Thr Glu Phe Asn Lys		
145	150	155 160
Ile Pro Leu Thr Ile Leu Ser Arg Cys Gln Ser Phe Phe Phe Lys Lys		
165	170	175

Ile Thr Ser Asp Leu Ile Leu Glu Arg Leu Asn Asp Ile Ala Lys Lys
 180 185 190
 Glu Lys Ile Lys Ile Glu Lys Asp Ala Leu Ile Lys Ile Ala Asp Leu
 195 200 205
 Ser Gln Gly Ser Leu Arg Asp Gly Leu Ser Leu Leu Asp Gln Leu Ala
 210 215 220
 Ile Ser Leu Ile Val Lys Lys Leu Val Leu Leu Met Leu Lys Lys His
 225 230 235 240
 Leu Ile Ser Leu Ile Glu Met Gln Asn Leu Leu Leu Leu Lys Gln Phe
 245 250 255
 Tyr Gln Glu Ile
 260

<210> 26
 <211> 289
 <212> PRT
 <213> Thermus thermophilus

<400> 26
 Val Ser Ala Leu Tyr Arg Arg Phe Arg Pro Leu Thr Phe Gln Glu Val
 1 5 10 15
 Val Gly Gln Glu His Val Lys Glu Pro Leu Leu Lys Ala Ile Arg Glu
 20 25 30
 Gly Arg Leu Ala Gln Ala Tyr Leu Phe Ser Gly Pro Arg Gly Val Gly
 35 40 45
 Lys Thr Thr Thr Ala Arg Leu Leu Ala Met Ala Val Gly Cys Gln Gly
 50 55 60
 Glu Asp Pro Pro Cys Gly Val Cys Pro His Cys Gln Ala Val Gln Arg
 65 70 75 80
 Gly Ala His Pro Asp Val Val Asp Ile Asp Ala Ala Ser Asn Asn Ser
 85 90 95
 Val Glu Asp Val Arg Glu Leu Arg Glu Arg Ile His Leu Ala Pro Leu
 100 105 110
 Ser Ala Pro Arg Lys Val Phe Ile Leu Asp Glu Ala His Met Leu Ser
 115 120 125

Lys Ser Ala Phe Asn Ala Leu Leu Lys Thr Leu Glu Glu Pro Pro Pro
 130 135 140

His Val Leu Phe Val Phe Ala Thr Thr Glu Pro Glu Arg Met Pro Pro
 145 150 155 160

Thr Ile Leu Ser Arg Thr Gln His Phe Arg Phe Arg Arg Leu Thr Glu
 165 170 175

Glu Glu Ile Ala Phe Lys Leu Arg Arg Ile Leu Glu Ala Val Gly Arg
 180 185 190

Glu Ala Glu Glu Glu Ala Leu Leu Leu Leu Ala Arg Leu Ala Asp Gly
 195 200 205

Ala Leu Arg Asp Ala Glu Ser Leu Leu Glu Arg Phe Leu Leu Leu Glu
 210 215 220

Gly Pro Leu Thr Arg Lys Glu Val Glu Arg Ala Leu Gly Ser Pro Pro
 225 230 235 240

Gly Thr Gly Val Ala Glu Ile Ala Ala Ser Leu Ala Arg Gly Lys Thr
 245 250 255

Ala Glu Ala Leu Gly Leu Ala Arg Arg Leu Tyr Gly Glu Gly Tyr Ala
 260 265 270

Pro Arg Ser Leu Val Ser Gly Leu Leu Glu Val Phe Arg Glu Gly Leu
 275 280 285

Tyr

<210> 27

<211> 101

<212> RNA

<213> Thermus thermophilus

<400> 27

guccuggagg gagaaaaaaa aagccugagc ccaaggcccc gcccggcccc accuccugaa 60
 gcgcccgcac ccccgggccc ucccgaggag gagguagagg c 101

<210> 28

<211> 11

<212> PRT

<213> Thermus thermophilus

<400> 28

Val Leu Glu Gly Glu Lys Lys Ser Leu Ser Pro
1 5 10

<210> 29

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<220>

<221> unsure

<222> (6)

<223> N at position 6 is either G or C

<220>

<221> unsure

<222> (12)

<223> N at position 12 is either G or C

<220>

<221> unsure

<222> (21)

<223> N at position 21 is either G or C

<400> 29

cacgcntacc tnttctccgg nac

23

<210> 30

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<220>

<221> unsure

<222> (7)

<223> N at position 7 is either G or C

<220>

<221> unsure
<222> (10)
<223> N at position 10 is either G or C

<220>
<221> unsure
<222> (19)
<223> N at position 19 is either G or C

<220>
<221> unsure
<222> (22)
<223> N at position 22 is either G or C

<400> 30
gtgctcnggn ggctcctcnt cngtc 25

<210> 31
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 31
gtgggatccg tggttctgga tctcgatgaa gaa 33

<210> 32
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 32
gtgggatcca cggsetstcs gagcagaag 29

<210> 33
<211> 34
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 33

gcgggatacct caacgaggac ctctccatct tcaa

34

<210> 34

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 34

gcgggatacct tgcgtcsag sgtsagsgcg tcgta

35

<210> 35

<211> 39

<212> DNA

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<220>

<223> Description of Artificial Sequence: primer

<400> 35

gggaaggacc agcgcgtact cccctgctc ctaggtgtg

39

<210> 36

<211> 27

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: primer

<400> 36

gtgtggatcc ttcttcttsc ccatsgc

27

<210> 37

<211> 27

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: primer

<400> 37

caccgattcc agtggtgcct aggtgtg

27

<210> 38

<211> 30

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: primer

<400> 38

caacacctg tgttcagga gcctgtgctt

30

<210> 39

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 39

ccagaatcgt ctgctggctg tag

23

<210> 40

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 40

agcaccctgg aggagcttc

19

<210> 41

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 41

catgtcgtac tgggtgtac

19

<210> 42

<211> 27

<212> DNA

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<223> Description of Artificial Sequence: primer

<220>

<221> unsure

<222> (7)

<223> N at position 7 is A, C, G, or T

<220>

<221> unsure

<222> (8)

<223> N at position 8 is A, C, G, or T

<220>

<221> unsure

<222> (13)

<223> N at position 13 is A, C, G, or T

<220>

<221> unsure

<222> (14)

<223> N at position 14 is A, C, G, or T

<400> 42

gtsgtsnsg acnnsagac sacsggg

27

<210> 43

<211> 27

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: primer

<220>

<221> unsure

<222> (8)
<223> N at position 8 is A, C, G, or T

<220>
<221> unsure
<222> (9)
<223> N at position 9 is A, C, G, or T

<220>
<221> unsure
<222> (17)
<223> N at position 17 is A, C, G, or T

<220>
<221> unsure
<222> (18)
<223> N at position 18 is A, C, G, or T

<400> 43
gaasccsnng tcgaasnngg cgttgtg 27

<210> 44
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 44
cggggatcca cctcaatcac ctctgtg 27

<210> 45
<211> 30
<212> DNA
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<220>
<223> Description of Artificial Sequence: primer

<400> 45
cggggatccg ccaccttgcg gctccgggtg 30

<210> 46
<211> 31

<212> DNA
 <213> Artificial Sequence

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 <223> Description of Artificial Sequence: primer

 <400> 46
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 <210> 47
 <211> 25
 <212> DNA
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 <400> 47
 cgcgtctaga tcacctgtat ccaga 25

 <210> 48
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 <212> DNA
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 <220>
 <223> Description of Artificial Sequence: primer

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 gcggcgcata tgggtggtggt cctggacctg gag 33

 <210> 49
 <211> 25
 <212> DNA
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 <400> 49
 cgcgtctaga tcacctgtat ccaga 25

 <210> 50
 <211> 20

<212> DNA
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 <220>
 <223> Description of Artificial Sequence: primer

 <400> 50
 gtsctsgtsa agacscactt 20

 <210> 51
 <211> 21
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 <223> Description of Artificial Sequence: primer

 <400> 51
 sagsagsgcg ttgaasgtgt g 21

 <210> 52
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 52
 ctcgttggtg aaagtttccg tg 22

 <210> 53
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 53
 cgtccagttc atcgccggaa agga 24

 <210> 54
 <211> 27

<212> DNA
 <213> Artificial Sequence

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 <223> Description of Artificial Sequence: primer

 <400> 54
 tctggcaaca cgttctggag cacatcc 27

 <210> 55
 <211> 23
 <212> DNA
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 <220>
 <223> Description of Artificial Sequence: primer

 <400> 55
 tgctggcgtt catcttcagg atg 23

 <210> 56
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 56
 catcctgaag atgaacgcca gca 23

 <210> 57
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 57
 aggttatcca caggggtcat gtgca 25

 <210> 58
 <211> 29

<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 58

gtgtgtcata tgaacataac ggttcccaa

29

<210> 59

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 59

gcgcgaattc tcccttgtag aaggcttag

29

<210> 60

<211> 13

<212> PRT

<213> Thermus thermophilus

<400> 60

Arg Val Glu Leu Asp Tyr Asp Ala Leu Thr Leu Asp Asp

1

5

10

<210> 61

<211> 14

<212> PRT

<213> Thermus thermophilus

<400> 61

Phe Phe Ile Glu Ile Gln Asn His Gly Leu Ser Glu Gln Lys

1

5

10

<210> 62

<211> 8

<212> PRT

<213> Thermus thermophilus

<400> 62

Phe Phe Ile Glu Ile Gln Asn His
1 5

<210> 63

<211> 8

<212> PRT

<213> Thermus thermophilus

<400> 63

Tyr Asp Ala Leu Thr Leu Asp Asp
1 5

<210> 64

<211> 6

<212> PRT

<213> Thermus thermophilus

<400> 64

Ala Met Gly Lys Lys Lys
1 5

<210> 65

<211> 9

<212> PRT

<213> Thermus thermophilus

<400> 65

Phe Asn Lys Ser His Ser Ala Ala Tyr
1 5

<210> 66

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: peptide

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<221> PEPTIDE

<222> (3)

<223> Xaa at position 3 is undefined

<220>

<221> PEPTIDE
<222> (5)
<223> Xaa at position 5 is undefined

<400> 66
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1 5

<210> 67
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<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: peptide

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<222> (4)
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<222> (7)
<223> Xaa at position 7 is undefined

<400> 67
His Asn Ala Xaa Phe Asp Xaa Gly Phe
1 5

<210> 68
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<212> PRT
<213> Artificial Sequence

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<221> PEPTIDE
<222> (5)

<223> Xaa at position 5 is undefined

<400> 68

Val Val Xaa Asp Xaa Glu Thr Thr Gly
1 5

<210> 69

<211> 7

<212> PRT

<213> *Thermus thermophilus*

<400> 69

Val Leu Val Lys Thr His Leu
1 5

<210> 70

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: peptide

<400> 70

His Arg Ala Leu Tyr Asp
1 5

<210> 71

<211> 7

<212> PRT

<213> *Thermus thermophilus*

<400> 71

His Thr Phe Asn Ala Leu Leu
1 5

<210> 72

<211> 34

<212> PRT

<213> *Escherichia coli*

<400> 72

Asp Arg Tyr Phe Leu Glu Leu Ile Arg Thr Gly Arg Pro Asp Glu Glu
1 5 10 15

Ser Tyr Leu His Ala Ala Val Glu Leu Ala Glu Ala Arg Gly Leu Pro
 20 25 30

Val Val

<210> 73

<211> 34

<212> PRT

<213> *Vibrio cholerae*

<400> 73

Asp His Phe Tyr Leu Glu Leu Ile Arg Thr Gly Arg Ala Asp Glu Glu
 1 5 10 15

Ser Tyr Leu His Phe Ala Leu Asp Val Ala Glu Gln Tyr Asp Leu Pro
 20 25 30

Val Val

<210> 74

<211> 34

<212> PRT

<213> *Haemophilus influenzae*

<400> 74

Asp His Phe Tyr Leu Ala Leu Ser Arg Thr Gly Arg Pro Asn Glu Glu
 1 5 10 15

Arg Tyr Ile Gln Ala Ala Leu Lys Leu Ala Glu Arg Cys Asp Leu Pro
 20 25 30

Leu Val

<210> 75

<211> 34

<212> PRT

<213> *Rickettsia prowazekii*

<400> 75

Asp Arg Phe Tyr Phe Glu Ile Met Arg His Asp Leu Pro Glu Glu Gln
 1 5 10 15

Phe Ile Glu Asn Ser Tyr Ile Gln Ile Ala Ser Glu Leu Ser Ile Pro
20 25 30

Ile Val

<210> 76

<211> 34

<212> PRT

<213> *Helicobacter pylori*

<400> 76

Asp Asp Phe Tyr Leu Glu Ile Met Arg His Gly Ile Leu Asp Gln Arg
1 5 10 15

Phe Ile Asp Glu Gln Val Ile Lys Met Ser Leu Glu Thr Gly Leu Lys
20 25 30

Ile Ile

<210> 77

<211> 34

<212> PRT

<213> *Synechocystis* sp.

<400> 77

Asp Asp Tyr Tyr Leu Glu Ile Gln Asp His Gly Ser Val Glu Asp Arg
1 5 10 15

Leu Val Asn Ile Asn Leu Val Lys Ile Ala Gln Glu Leu Asp Ile Lys
20 25 30

Ile Val

<210> 78

<211> 34

<212> PRT

<213> *Mycobacterium tuberculosis*

<400> 78

Asp Asn Tyr Phe Leu Glu Leu Met Asp His Gly Leu Thr Ile Glu Arg
1 5 10 15

Arg Val Arg Asp Gly Leu Leu Glu Ile Gly Arg Ala Leu Asn Ile Pro
 20 25 30

Pro Leu

<210> 79

<211> 46

<212> PRT

<213> Escherichia coli

<400> 79

Asn Lys Arg Arg Ala Lys Asn Gly Glu Pro Pro Leu Asp Ile Ala Ala
 1 5 10 15

Ile Pro Leu Asp Asp Lys Lys Ser Phe Asp Met Leu Gln Arg Ser Glu
 20 25 30

Thr Thr Ala Val Phe Gln Leu Glu Ser Arg Gly Met Lys Asp
 35 40 45

<210> 80

<211> 46

<212> PRT

<213> Vibrio cholerae

<400> 80

Asn Pro Arg Leu Lys Lys Ala Gly Lys Pro Pro Val Arg Ile Glu Ala
 1 5 10 15

Ile Pro Leu Asp Asp Ala Arg Ser Phe Arg Asn Leu Gln Asp Ala Lys
 20 25 30

Thr Thr Ala Val Phe Gln Leu Glu Ser Arg Gly Met Lys Glu
 35 40 45

<210> 81

<211> 46

<212> PRT

<213> Haemophilus influenzae

<400> 81

Asn Val Arg Met Val Arg Glu Gly Lys Pro Arg Val Asp Ile Ala Ala
 1 5 10 15

Ile Pro Leu Asp Asp Pro Glu Ser Phe Glu Leu Leu Lys Arg Ser Glu
20 25 30

Thr Thr Ala Val Phe Gln Leu Glu Ser Arg Gly Met Lys Asp
35 40 45

<210> 82

<211> 46

<212> PRT

<213> Rickettsia prowazekii

<400> 82

Cys Lys Lys Leu Leu Lys Glu Gln Gly Ile Lys Ile Asp Phe Asp Asp
1 5 10 15

Met Thr Phe Asp Asp Lys Lys Thr Tyr Gln Met Leu Cys Lys Gly Lys
20 25 30

Gly Val Gly Val Phe Gln Phe Glu Ser Ile Gly Met Lys Asp
35 40 45

<210> 83

<211> 45

<212> PRT

<213> Helicobacter pylori

<400> 83

Leu Lys Ile Ile Lys Thr Gln His Lys Ile Ser Val Asp Phe Leu Ser
1 5 10 15

Leu Asp Met Asp Asp Pro Lys Val Tyr Lys Thr Ile Gln Ser Gly Asp
20 25 30

Thr Val Gly Ile Phe Gln Ile Glu Ser Gly Met Phe Gln
35 40 45

<210> 84

<211> 46

<212> PRT

<213> Synechocystis sp.

<400> 84

Gln Glu Arg Lys Ala Leu Gln Ile Arg Ala Arg Thr Gly Ser Lys Lys
1 5 10 15

Leu Pro Asp Asp Val Lys Lys Thr His Lys Leu Leu Glu Ala Gly Asp
20 25 30

Leu Glu Gly Ile Phe Gln Leu Glu Ser Gln Gly Met Lys Gln
35 40 45

<210> 85

<211> 46

<212> PRT

<213> Mycobacterium tuberculosis

<400> 85

Ile Asp Asn Val Arg Ala Asn Arg Gly Ile Asp Leu Asp Leu Glu Ser
1 5 10 15

Val Pro Leu Asp Asp Lys Ala Thr Tyr Glu Leu Leu Gly Arg Gly Asp
20 25 30

Thr Leu Gly Val Phe Gln Leu Asp Gly Gly Pro Met Arg Asp
35 40 45

<210> 86

<211> 3729

<212> DNA

<213> Thermus thermophilus

<400> 86

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gccttgGCCa tgaccgacca cggcaacctc ttcggggccg tggagttcta caagaaggcc 180
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gcccgcgccc acgaggtcct cctcgccatc cagtccaaga gcacctgga cgaccccggg 720
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cgctaccggg accggatcac cgagggttc taccgggagg tcttccgcct tttggggaag 1020
cttccccccc acggggacgg ggaggccttg gccgaggcct tggcccaggt ggagcgggag 1080

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cccttttgg						3729

<211> 1245

<212> PRT

<213> *Thermus thermophilus*

<400> 87

Met Gly Arg Glu Leu Arg Phe Ala His Leu His Gln His Thr Gln Phe
1 5 10 15

Ser Leu Leu Asp Gly Ala Pro Lys Leu Ser Asp Leu Leu Lys Trp Val
20 25 30

Glu Glu Thr Thr Pro Glu Asp Pro Ala Leu Ala Met Thr Asp His Gly
35 40 45

Asn Leu Phe Gly Ala Val Glu Phe Tyr Lys Lys Ala Thr Glu Met Gly
50 55 60

Ile Lys Pro Ile Leu Gly Tyr Glu Ala Tyr Val Ala Ala Glu Ser Arg
65 70 75 80

Phe Asp Arg Lys Arg Gly Lys Gly Leu Asp Gly Gly Tyr Phe His Leu
85 90 95

Thr Leu Leu Ala Lys Asp Phe Thr Gly Tyr Gln Asn Leu Val Arg Leu
100 105 110

Ala Ser Arg Ala Tyr Leu Glu Gly Phe Tyr Glu Lys Pro Arg Ile Asp
115 120 125

Arg Glu Ile Leu Arg Glu His Ala Glu Gly Leu Ile Ala Leu Ser Gly
130 135 140

Cys Leu Gly Ala Glu Ile Pro Gln Phe Ile Leu Gln Asp Arg Leu Asp
145 150 155 160

Leu Ala Glu Ala Arg Leu Asn Glu Tyr Leu Ser Ile Phe Lys Asp Arg
165 170 175

Phe Phe Ile Glu Ile Gln Asn His Gly Leu Pro Glu Gln Lys Lys Val
180 185 190

Asn Glu Val Leu Lys Glu Phe Ala Arg Lys Tyr Gly Leu Gly Met Val
195 200 205

Ala Thr Asn Asp Gly His Tyr Val Arg Lys Glu Asp Ala Arg Ala His
210 215 220

Glu Val Leu Leu Ala Ile Gln Ser Lys Ser Thr Leu Asp Asp Pro Gly

225		230		235		240									
Ala	Leu	Ala	Leu	Pro	Cys	Glu	Glu	Phe	Tyr	Val	Lys	Thr	Pro	Glu	Glu
				245					250					255	
Met	Arg	Ala	Met	Phe	Pro	Glu	Glu	Glu	Val	Gly	Gly	Arg	Ser	Pro	Leu
			260					265					270		
Thr	Thr	Pro	Trp	Arg	Ser	Pro	His	Val	Gln	Arg	Gly	Ala	Ala	Ile	Gly
		275					280					285			
Thr	Arg	Trp	Ser	Thr	Arg	Ile	Pro	Arg	Phe	Pro	Leu	Pro	Glu	Gly	Arg
	290					295					300				
Thr	Glu	Ala	Gln	Tyr	Leu	Met	Glu	Leu	Thr	Phe	Lys	Gly	Leu	Leu	Arg
305					310					315					320
Arg	Tyr	Pro	Asp	Arg	Ile	Thr	Glu	Gly	Phe	Tyr	Arg	Glu	Val	Phe	Arg
				325					330					335	
Leu	Ser	Gly	Lys	Leu	Pro	Pro	His	Gly	Asp	Gly	Glu	Ala	Leu	Ala	Glu
			340					345					350		
Ala	Leu	Ala	Gln	Val	Glu	Arg	Glu	Ala	Trp	Glu	Arg	Leu	Met	Lys	Ser
		355					360					365			
Leu	Pro	Pro	Leu	Ala	Gly	Val	Lys	Glu	Trp	Thr	Ala	Glu	Ala	Ile	Phe
	370					375					380				
His	Arg	Ala	Leu	Tyr	Glu	Leu	Ser	Ala	Ile	Glu	Arg	Met	Gly	Phe	Pro
385					390					395					400
Gly	Leu	Leu	Pro	His	Arg	Pro	Gly	Leu	His	Gln	Leu	Gly	Pro	Glu	Lys
				405					410					415	
Gly	Val	Ser	Val	Gly	Pro	Gly	Arg	Gly	Gly	Ala	Ala	Gly	Ser	Leu	Val
			420					425					430		
Ala	Tyr	Ala	Val	Gly	Ile	Thr	Asn	Ile	Asp	Pro	Leu	Arg	Phe	Gly	Leu
		435					440					445			
Leu	Phe	Glu	Arg	Phe	Leu	Asn	Pro	Glu	Arg	Val	Ser	Met	Pro	Asp	Ile
	450					455					460				
Asp	Thr	Asp	Phe	Ser	Asp	Arg	Glu	Arg	Asp	Arg	Val	Ile	Gln	Tyr	Val
465					470					475					480
Arg	Glu	Arg	Tyr	Gly	Glu	Asp	Lys	Val	Ala	Gln	Ile	Gly	Thr	Leu	Gly

485					490					495					
Ser	Leu	Ala	Ser	Lys	Ala	Ala	Leu	Lys	Glu	Val	Ala	Arg	Val	Tyr	Gly
			500					505					510		
Ile	Pro	Arg	Lys	Lys	Ala	Glu	Glu	Leu	Ala	Lys	Leu	Ile	Pro	Val	Gln
			515				520					525			
Phe	Gly	Lys	Pro	Lys	Pro	Leu	Gln	Glu	Ala	Ile	Gln	Val	Val	Pro	Glu
	530					535					540				
Leu	Arg	Ala	Glu	Met	Glu	Lys	Asp	Pro	Lys	Val	Arg	Glu	Val	Leu	Glu
545						550					555				560
Val	Ala	Met	Arg	Leu	Glu	Gly	Leu	Asn	Arg	His	Ala	Ser	Val	His	Ala
				565					570					575	
Gly	Arg	Gly	Gly	Val	Phe	Ser	Glu	Pro	Leu	Thr	Asp	Leu	Val	Pro	Leu
			580					585					590		
Cys	Ala	Thr	Arg	Lys	Gly	Gly	Pro	Tyr	Thr	Gln	Tyr	Asp	Met	Gly	Ala
			595				600					605			
Val	Glu	Ala	Leu	Gly	Leu	Leu	Lys	Met	Asp	Phe	Leu	Gly	Leu	Arg	Thr
	610					615					620				
Leu	Thr	Phe	Leu	Asp	Glu	Val	Lys	Arg	Ile	Val	Lys	Ala	Ser	Gln	Gly
625						630					635				640
Val	Glu	Leu	Asp	Tyr	Asp	Ala	Leu	Pro	Leu	Asp	Asp	Pro	Lys	Thr	Phe
				645					650					655	
Ala	Leu	Leu	Ser	Arg	Gly	Glu	Thr	Lys	Gly	Val	Phe	Gln	Leu	Glu	Ser
			660					665					670		
Gly	Gly	Met	Thr	Ala	Thr	Leu	Arg	Gly	Leu	Lys	Pro	Arg	Arg	Phe	Glu
		675					680					685			
Asp	Leu	Ile	Ala	Ile	Leu	Ser	Leu	Tyr	Arg	Pro	Gly	Pro	Met	Glu	His
	690					695					700				
Ile	Pro	Thr	Tyr	Ile	Arg	Arg	His	His	Gly	Leu	Glu	Pro	Val	Ser	Tyr
705						710					715				720
Ser	Glu	Phe	Pro	His	Ala	Glu	Lys	Tyr	Leu	Lys	Pro	Ile	Leu	Asp	Glu
				725					730					735	
Thr	Tyr	Gly	Ile	Pro	Val	Tyr	Gln	Glu	Gln	Ile	Met	Gln	Ile	Ala	Ser

740	745	750
Ala Val Ala Gly Tyr Ser Leu Gly Glu Ala Asp Leu Leu Arg Arg Ser		
755	760	765
Met Gly Lys Lys Lys Val Glu Glu Met Lys Ser His Arg Glu Arg Phe		
770	775	780
Val Gln Gly Ala Lys Glu Arg Gly Val Pro Glu Glu Glu Ala Asn Arg		
785	790	795
800		
Leu Phe Asp Met Leu Glu Ala Phe Ala Asn Tyr Gly Phe Asn Lys Ser		
805	810	815
His Ala Ala Ala Tyr Ser Leu Leu Ser Tyr Gln Thr Ala Tyr Val Lys		
820	825	830
Ala His Tyr Pro Val Glu Phe Met Ala Ala Leu Leu Ser Val Glu Arg		
835	840	845
His Asp Ser Asp Lys Val Ala Glu Tyr Ile Arg Asp Ala Arg Ala Met		
850	855	860
Gly Ile Glu Val Leu Pro Pro Asp Val Asn Arg Ser Gly Phe Asp Phe		
865	870	875
880		
Leu Val Gln Gly Arg Gln Ile Leu Phe Gly Leu Ser Ala Val Lys Asn		
885	890	895
Val Gly Glu Ala Ala Ala Glu Ala Ile Leu Arg Glu Arg Glu Arg Gly		
900	905	910
Gly Pro Tyr Arg Ser Leu Gly Asp Phe Leu Lys Arg Leu Asp Glu Lys		
915	920	925
Val Leu Asn Lys Arg Thr Leu Glu Ser Leu Ile Lys Ala Gly Ala Leu		
930	935	940
Asp Gly Phe Gly Glu Arg Ala Arg Leu Leu Ala Ser Leu Glu Gly Leu		
945	950	955
960		
Leu Lys Trp Ala Ala Glu Asn Arg Glu Lys Ala Arg Ser Gly Met Met		
965	970	975
Gly Leu Phe Ser Glu Val Glu Glu Pro Pro Leu Ala Glu Ala Ala Pro		
980	985	990
Leu Asp Glu Ile Thr Arg Leu Arg Tyr Glu Lys Glu Ala Leu Gly Ile		

995	1000	1005
Tyr Val Ser Gly His Pro Ile Leu Arg Tyr Pro Gly Leu Arg Glu Thr		
1010	1015	1020
Ala Thr Cys Thr Leu Glu Glu Leu Pro His Leu Ala Arg Asp Leu Pro		
1025	1030	1035 1040
Pro Arg Ser Arg Val Leu Leu Ala Gly Met Val Glu Glu Val Val Arg		
	1045	1050 1055
Lys Pro Thr Lys Ser Gly Gly Met Met Ala Arg Phe Val Leu Ser Asp		
	1060	1065 1070
Glu Thr Gly Ala Leu Glu Ala Val Ala Phe Gly Arg Ala Tyr Asp Gln		
	1075	1080 1085
Val Ser Pro Arg Leu Lys Glu Asp Thr Pro Val Leu Val Leu Ala Glu		
	1090	1095 1100
Val Glu Arg Glu Glu Gly Gly Val Arg Val Leu Ala Gln Ala Val Trp		
1105	1110	1115 1120
Thr Tyr Gln Glu Leu Glu Gln Val Pro Arg Ala Leu Glu Val Glu Val		
	1125	1130 1135
Glu Ala Ser Leu Pro Asp Asp Arg Gly Val Ala His Leu Lys Ser Leu		
	1140	1145 1150
Leu Asp Glu His Ala Gly Thr Leu Pro Leu Tyr Val Arg Val Gln Gly		
	1155	1160 1165
Ala Phe Gly Glu Ala Leu Leu Ala Leu Arg Glu Val Arg Val Gly Glu		
	1170	1175 1180
Glu Ala Leu Gly Ala Leu Glu Ala Ala Gly Phe Pro Ala Tyr Leu Leu		
1185	1190	1195 1200
Pro Asn Arg Glu Val Ser Pro Arg Leu Thr Gly Ser Gly Gly Pro Arg		
	1205	1210 1215
Gly Arg Ala Leu Ser Thr Gly Leu Ala Leu Lys Thr Tyr Pro Ile Ala		
	1220	1225 1230
Leu Pro Gly Gly Asn Glu Ala Leu Ala Arg Pro Leu Leu		
	1235	1240 1245

<210> 88
 <211> 198
 <212> PRT
 <213> *Thermus thermophilus*

<400> 88

Val	Glu	Arg	Val	Val	Arg	Thr	Leu	Leu	Asp	Gly	Arg	Phe	Leu	Leu	Glu
1				5					10					15	
Glu	Gly	Val	Gly	Leu	Trp	Glu	Trp	Arg	Tyr	Pro	Phe	Pro	Leu	Glu	Gly
		20						25					30		
Glu	Ala	Val	Val	Val	Leu	Asp	Leu	Glu	Thr	Thr	Gly	Leu	Ala	Gly	Leu
		35						40				45			
Asp	Glu	Val	Ile	Glu	Val	Gly	Leu	Leu	Arg	Leu	Glu	Gly	Gly	Arg	Arg
	50					55					60				
Leu	Pro	Phe	Gln	Ser	Leu	Val	Arg	Pro	Leu	Pro	Pro	Ala	Glu	Ala	Arg
65					70					75					80
Ser	Trp	Asn	Leu	Thr	Gly	Ile	Pro	Arg	Glu	Ala	Leu	Glu	Glu	Ala	Pro
				85					90					95	
Ser	Leu	Glu	Glu	Val	Leu	Glu	Lys	Ala	Tyr	Pro	Leu	Arg	Gly	Asp	Ala
		100						105					110		
Thr	Leu	Val	Ile	His	Asn	Ala	Ala	Phe	Asp	Leu	Gly	Phe	Leu	Arg	Pro
		115					120					125			
Ala	Leu	Glu	Gly	Leu	Gly	Tyr	Arg	Leu	Glu	Asn	Pro	Val	Val	Asp	Ser
	130					135					140				
Leu	Arg	Leu	Ala	Arg	Arg	Gly	Leu	Pro	Gly	Leu	Arg	Arg	Tyr	Gly	Leu
145					150					155					160
Asp	Ala	Leu	Ser	Glu	Val	Leu	Glu	Leu	Pro	Arg	Arg	Thr	Cys	His	Arg
				165					170					175	
Ala	Leu	Glu	Asp	Val	Glu	Arg	Thr	Leu	Ala	Val	Val	His	Glu	Val	Tyr
		180						185					190		
Tyr	Met	Leu	Thr	Ser	Gly										
		195													

<210> 89
 <211> 182

<212> PRT

<213> *Deinococcus radiodurans*

<220>

<221> PEPTIDE

<222> (79)

<223> X at position 79 is undefined

<400> 89

Pro Trp Pro Gln Asp Val Val Val Phe Asp Leu Glu Thr Thr Gly Phe
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Ser Pro Ala Ser Ala Ala Ile Val Glu Ile Gly Ala Val Arg Ile Val
20 25 30

Gly Gly Gln Ile Asp Glu Thr Leu Lys Phe Glu Thr Leu Val Arg Pro
35 40 45

Thr Arg Pro Asp Gly Ser Met Leu Ser Ile Pro Trp Gln Ala Gln Arg
50 55 60

Val His Gly Ile Ser Asp Glu Met Val Arg Arg Ala Pro Ala Xaa Lys
65 70 75 80

Asp Val Leu Pro Asp Phe Phe Asp Phe Val Asp Gly Ser Ala Val Val
85 90 95

Ala His Asn Val Ser Phe Asp Gly Gly Phe Met Arg Ala Gly Ala Glu
100 105 110

Arg Leu Gly Leu Ser Trp Ala Pro Glu Arg Glu Leu Cys Thr Met Gln
115 120 125

Leu Ser Arg Arg Ala Phe Pro Arg Glu Arg Thr His Asn Leu Thr Val
130 135 140

Leu Ala Glu Arg Leu Gly Leu Glu Phe Ala Pro Gly Gly Arg His Arg
145 150 155 160

Ser Tyr Gly Asp Val Gln Val Thr Ala Gln Ala Tyr Leu Arg Leu Leu
165 170 175

Glu Leu Leu Gly Glu Arg
180

<210> 90

<211> 201

<212> PRT

<213> *Bacillus subtilis*

<400> 90

His Gly Ile Lys Met Ile Tyr Gly Met Glu Ala Asn Leu Val Asp Asp
1 5 10 15

Gly Val Pro Ile Ala Tyr Asn Ala Ala His Arg Leu Leu Glu Glu Glu
20 25 30

Thr Tyr Val Val Phe Asp Val Glu Thr Thr Gly Leu Ser Ala Val Tyr
35 40 45

Asp Thr Ile Ile Glu Leu Ala Ala Val Lys Val Lys Gly Gly Glu Ile
50 55 60

Ile Asp Lys Phe Glu Ala Phe Ala Asn Pro His Arg Pro Leu Ser Ala
65 70 75 80

Thr Ile Ile Glu Leu Thr Gly Ile Thr Asp Asp Met Leu Gln Asp Ala
85 90 95

Pro Asp Val Val Asp Val Ile Arg Asp Phe Arg Glu Trp Ile Gly Asp
100 105 110

Asp Ile Leu Val Ala His Asn Ala Ser Phe Asp Met Gly Phe Leu Asn
115 120 125

Val Ala Tyr Lys Lys Leu Leu Glu Val Glu Lys Ala Lys Asn Pro Val
130 135 140

Ile Asp Thr Leu Glu Leu Gly Arg Phe Leu Tyr Pro Glu Phe Lys Asn
145 150 155 160

His Arg Leu Asn Thr Leu Cys Lys Lys Phe Asp Ile Glu Leu Thr Gln
165 170 175

His His Arg Ala Ile Tyr Asp Thr Glu Ala Thr Ala Tyr Leu Leu Leu
180 185 190

Lys Met Leu Lys Asp Ala Ala Glu Lys
195 200

<210> 91

<211> 188

<212> PRT

<213> *Haemophilus influenzae*

<220>
 <221> PEPTIDE
 <222> (47)
 <223> X at position 47 is undefined

<220>
 <221> PEPTIDE
 <222> (57)
 <223> X at position 57 is undefined

<400> 91
 Met Ile Asn Pro Asn Arg Gln Ile Val Leu Asp Thr Glu Thr Thr Gly
 1 5 10 15
 Met Asn Gln Leu Gly Ala His Tyr Glu Gly His Cys Ile Ile Glu Ile
 20 25 30
 Gly Ala Val Glu Leu Ile Asn Arg Arg Tyr Thr Gly Asn Asn Xaa His
 35 40 45
 Ile Tyr Ile Lys Pro Asp Arg Pro Xaa Asp Pro Asp Ala Ile Lys Val
 50 55 60
 His Gly Ile Thr Asp Glu Met Leu Ala Asp Lys Pro Glu Phe Lys Glu
 65 70 75 80
 Val Ala Gln Asp Phe Leu Asp Tyr Ile Asn Gly Ala Glu Leu Leu Ile
 85 90 95
 His Asn Ala Pro Phe Asp Val Gly Phe Met Asp Tyr Glu Phe Arg Lys
 100 105 110
 Leu Asn Leu Asn Val Lys Thr Asp Asp Ile Cys Leu Val Thr Asp Thr
 115 120 125
 Leu Gln Met Ala Arg Gln Met Tyr Pro Gly Lys Arg Asn Asn Leu Asp
 130 135 140
 Ala Leu Cys Asp Arg Leu Gly Ile Asp Asn Ser Lys Arg Thr Leu His
 145 150 155 160
 Gly Ala Leu Leu Asp Ala Glu Ile Leu Ala Asp Val Tyr Leu Met Met
 165 170 175
 Thr Gly Gly Gln Thr Asn Leu Phe Asp Glu Glu Glu
 180 185

<210> 92
 <211> 189
 <212> PRT
 <213> Escherichia coli

<400> 92

Met	Ser	Thr	Ala	Ile	Thr	Arg	Gln	Ile	Val	Leu	Asp	Thr	Glu	Thr	Thr
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Gly	Met	Asn	Gln	Ile	Gly	Ala	His	Ser	Glu	Gly	His	Lys	Ile	Ile	Glu
			20					25					30		
Ile	Gly	Ala	Val	Glu	Val	Val	Asn	Arg	Arg	Leu	Thr	Gly	Asn	Asn	Phe
		35					40					45			
His	Val	Tyr	Leu	Lys	Asp	Arg	Leu	Val	Asp	Pro	Glu	Ala	Phe	Gly	Val
	50					55					60				
His	Gly	Ile	Ala	Val	Asp	Phe	Leu	Leu	Asp	Lys	Pro	Thr	Phe	Ala	Glu
65					70					75					80
Val	Ala	Val	Glu	Phe	Met	Asp	Tyr	Ile	Arg	Gly	Ala	Glu	Leu	Val	Ile
				85					90					95	
His	Asn	Ala	Ala	Phe	Asp	Ile	Gly	Phe	Met	Asp	Tyr	Glu	Phe	Ser	Leu
		100						105					110		
Leu	Lys	Arg	Asp	Ile	Ala	Lys	Thr	Asn	Thr	Phe	Cys	Lys	Val	Thr	Asp
		115					120					125			
Ser	Leu	Ala	Val	Ala	Arg	Lys	Met	Phe	Pro	Gly	Lys	Arg	Asn	Ser	Leu
	130					135					140				
Asp	Ala	Leu	Cys	Ala	Arg	Tyr	Glu	Ile	Asp	Asn	Ser	Lys	Arg	Thr	Leu
145					150					155					160
His	Gly	Ala	Leu	Leu	Asp	Ala	Gln	Ile	Leu	Ala	Glu	Val	Tyr	Leu	Ala
				165					170					175	
Met	Thr	Gly	Gly	Gln	Thr	Ser	Met	Ala	Phe	Ala	Met	Glu			
			180					185							

<210> 93
 <211> 201
 <212> PRT
 <213> Helicobacter pylori

<400> 93

Asn Leu Glu Tyr Leu Lys Ala Cys Gly Leu Asn Phe Ile Glu Thr Ser
1 5 10 15

Glu Asn Leu Ile Thr Leu Lys Asn Leu Lys Thr Pro Leu Lys Asp Glu
20 25 30

Val Phe Ser Phe Ile Asp Leu Glu Thr Thr Gly Ser Cys Pro Ile Lys
35 40 45

His Glu Ile Leu Glu Ile Gly Ala Val Gln Val Lys Gly Gly Glu Ile
50 55 60

Ile Asn Arg Phe Glu Thr Leu Val Lys Val Lys Ser Val Pro Asp Tyr
65 70 75 80

Ile Ala Glu Leu Thr Gly Ile Thr Tyr Glu Asp Thr Leu Asn Ala Pro
85 90 95

Ser Ala His Glu Ala Leu Gln Glu Leu Arg Leu Phe Leu Gly Asn Ser
100 105 110

Val Phe Val Ala His Asn Ala Asn Phe Asp Tyr Asn Phe Leu Gly Arg
115 120 125

Tyr Phe Val Glu Lys Leu His Cys Pro Leu Leu Asn Leu Lys Leu Cys
130 135 140

Thr Leu Asp Leu Ser Lys Arg Ala Ile Leu Ser Met Arg Tyr Ser Leu
145 150 155 160

Ser Phe Leu Lys Glu Leu Leu Gly Phe Gly Ile Glu Val Ser His Arg
165 170 175

Ala Tyr Ala Asp Ala Leu Ala Ser Tyr Lys Leu Phe Glu Ile Cys Leu
180 185 190

Leu Asn Leu Pro Ser Tyr Ile Lys Thr
195 200

<210> 94

<211> 630

<212> DNA

<213> *Thermus thermophilus*

<400> 94

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atggtggagc ggggtggtgcg gacccttctg gacgggaggt tcctcctgga ggaggggggtg 60
gggctttggg agtggcgcta cccctttccc ctggaggggg aggcggtggt ggtcctggac 120
ctggagacca cggggcttgc cggcctggac gaggtgattg aggtgggcct cctccgctg 180
gaggggggga ggcgctccc cttccagagc ctcgctcggc ccctcccgcc cgccgaagcc 240
cgttcgtgga acctcacgg catcccccg gagggcctgg aggaggcccc ctccctggag 300
gaggttctgga agaaggccta cccctccgc ggcgacgcca ccttggtgat ccacaacgcc 360
gcctttgacc tgggcttct cgcgccggcc ttggagggcc tgggctaccg cctggaaaac 420
cccgtggtgg actccctgcg cttggccaga cggggcttac caggccttag gcgctacggc 480
ctggacgccc tctccgaggt cctggagctt ccccggaagga cctgccaccg ggccctcgag 540
gacgtggagc gcaccctcgc cgtggtgcac gaggtatact atatgcttac gtccggccgt 600
ccccgcacgc tttgggaact cgggaggtag 630

```

<210> 95

<211> 210

<212> PRT

<213> *Thermus thermophilus*

<400> 95

```

Met Val Glu Arg Val Val Arg Thr Leu Leu Asp Gly Arg Phe Leu Leu
  1              5              10              15

```

```

Glu Glu Gly Val Gly Leu Trp Glu Trp Arg Tyr Pro Phe Pro Leu Glu
      20              25              30

```

```

Gly Glu Ala Val Val Val Leu Asp Leu Glu Thr Thr Gly Leu Ala Gly
      35              40              45

```

```

Leu Asp Glu Val Ile Glu Val Gly Leu Leu Arg Leu Glu Gly Gly Arg
      50              55              60

```

```

Arg Leu Pro Phe Gln Ser Leu Val Arg Pro Leu Pro Pro Ala Glu Ala
      65              70              75              80

```

```

Arg Ser Trp Asn Leu Thr Gly Ile Pro Arg Glu Ala Leu Glu Glu Ala
      85              90              95

```

```

Pro Ser Leu Glu Glu Val Leu Glu Lys Ala Tyr Pro Leu Arg Gly Asp
      100             105             110

```

```

Ala Thr Leu Val Ile His Asn Ala Ala Phe Asp Leu Gly Phe Leu Arg
      115             120             125

```

```

Pro Ala Leu Glu Gly Leu Gly Tyr Arg Leu Glu Asn Pro Val Val Asp
      130             135             140

```

```

Ser Leu Arg Leu Ala Arg Arg Gly Leu Pro Gly Leu Arg Arg Tyr Gly
      145             150             155             160

```

Leu Asp Ala Leu Ser Glu Val Leu Glu Leu Pro Arg Arg Thr Cys His
165 170 175

Arg Ala Leu Glu Asp Val Glu Arg Thr Leu Ala Val Val His Glu Val
180 185 190

Tyr Tyr Met Leu Thr Ser Gly Arg Pro Arg Thr Leu Trp Glu Leu Gly
195 200 205

Arg Glx
210

<210> 96

<211> 461

<212> PRT

<213> Pseudomonas marcesans

<400> 96

Met Leu Glu Ala Ser Trp Glu Lys Val Gln Ser Ser Leu Lys Gln Asn
1 5 10 15

Leu Ser Lys Pro Ser Tyr Glu Thr Trp Ile Arg Pro Thr Glu Phe Ser
20 25 30

Gly Phe Lys Asn Gly Glu Leu Thr Leu Ile Ala Pro Asn Ser Phe Ser
35 40 45

Ser Ala Trp Leu Lys Asn Asn Tyr Ser Gln Thr Ile Gln Glu Thr Ala
50 55 60

Glu Glu Ile Phe Gly Glu Pro Val Thr Val His Val Lys Val Lys Ala
65 70 75 80

Asn Ala Glu Ser Ser Asp Glu His Tyr Ser Ser Ala Pro Ile Thr Pro
85 90 95

Pro Leu Glu Ala Ser Pro Gly Ser Val Asp Ser Ser Gly Ser Ser Leu
100 105 110

Arg Leu Ser Lys Lys Thr Leu Pro Leu Leu Asn Leu Arg Tyr Val Phe
115 120 125

Asn Arg Phe Val Val Gly Pro Asn Ser Arg Met Ala His Ala Ala Ala
130 135 140

Met Ala Val Ala Glu Ser Pro Gly Arg Glu Phe Asn Pro Leu Phe Ile

145		150		155		160
Cys Gly Gly Val Gly Leu Gly Lys Thr His Leu Met Gln Ala Ile Gly						
	165		170		175	
His Tyr Arg Leu Glu Ile Asp Pro Gly Ala Lys Val Ser Tyr Val Ser						
	180		185		190	
Thr Glu Thr Phe Thr Asn Asp Leu Ile Leu Ala Ile Arg Gln Asp Arg						
	195		200		205	
Met Gln Ala Phe Arg Asp Arg Tyr Arg Ala Ala Asp Leu Ile Leu Val						
	210		215		220	
Asp Asp Ile Gln Phe Ile Glu Gly Lys Glu Tyr Thr Gln Glu Glu Phe						
225		230		235		240
Phe His Thr Phe Asn Ala Leu His Asp Ala Gly Ser Gln Ile Val Leu						
	245		250		255	
Ala Ser Asp Arg Pro Pro Ser Gln Ile Pro Arg Leu Gln Glu Arg Leu						
	260		265		270	
Met Ser Arg Phe Ser Met Gly Leu Ile Ala Asp Val Gln Ala Pro Asp						
	275		280		285	
Leu Glu Thr Arg Met Ala Ile Leu Gln Lys Lys Ala Glu His Glu Arg						
	290		295		300	
Val Gly Leu Pro Arg Asp Leu Ile Gln Phe Ile Ala Gly Arg Phe Thr						
305		310		315		320
Ser Asn Ile Arg Glu Leu Glu Gly Ala Leu Thr Arg Ala Ile Ala Phe						
	325		330		335	
Ala Ser Ile Thr Gly Leu Pro Met Thr Val Asp Ser Ile Ala Pro Met						
	340		345		350	
Leu Asp Pro Asn Gly Gln Gly Val Glu Val Thr Pro Lys Gln Val Leu						
	355		360		365	
Asp Lys Val Ala Glu Val Phe Lys Val Thr Pro Asp Glu Met Arg Ser						
	370		375		380	
Ala Ser Arg Arg Arg Pro Val Ser Gln Ala Arg Gln Val Gly Met Tyr						
385		390		395		400
Leu Met Arg Gln Gly Thr Asn Leu Ser Leu Pro Arg Ile Gly Asp Thr						

Ala	His	Tyr	Arg	Leu	Glu	Met	Tyr	Pro	Asn	Ala	Lys	Val	Tyr	Tyr	Val	165	170	175
Ser	Thr	Glu	Arg	Phe	Thr	Asn	Asp	Leu	Ile	Thr	Ala	Ile	Arg	Gln	Asp	180	185	190
Asn	Met	Glu	Asp	Phe	Arg	Ser	Tyr	Tyr	Arg	Ser	Ala	Asp	Phe	Leu	Leu	195	200	205
Ile	Asp	Asp	Ile	Gln	Phe	Ile	Lys	Gly	Lys	Glu	Tyr	Thr	Gln	Glu	Glu	210	215	220
Phe	Phe	His	Thr	Phe	Asn	Ser	Leu	His	Glu	Ala	Gly	Lys	Gln	Val	Val	225	230	235
Val	Ala	Ser	Asp	Arg	Ala	Pro	Gln	Arg	Ile	Pro	Gly	Leu	Gln	Asp	Arg	245	250	255
Leu	Ile	Ser	Arg	Phe	Ser	Met	Gly	Leu	Ile	Ala	Asp	Ile	Gln	Val	Pro	260	265	270
Asp	Leu	Glu	Thr	Arg	Met	Ala	Ile	Leu	Gln	Lys	Lys	Ala	Glu	Tyr	Asp	275	280	285
Arg	Ile	Arg	Leu	Pro	Lys	Glu	Val	Ile	Glu	Tyr	Ile	Ala	Ser	His	Tyr	290	295	300
Thr	Ser	Asn	Ile	Arg	Glu	Leu	Glu	Gly	Ala	Leu	Ile	Arg	Ala	Ile	Ala	305	310	315
Tyr	Thr	Ser	Leu	Ser	Asn	Val	Ala	Met	Thr	Val	Glu	Asn	Ile	Ala	Pro	325	330	335
Val	Leu	Asn	Pro	Pro	Val	Glu	Lys	Val	Ala	Ala	Ala	Pro	Glu	Thr	Ile	340	345	350
Ile	Thr	Ile	Val	Ala	Gln	His	Tyr	Gln	Leu	Lys	Val	Glu	Glu	Leu	Leu	355	360	365
Ser	Asn	Ser	Arg	Arg	Arg	Glu	Val	Ser	Leu	Ala	Arg	Gln	Val	Gly	Met	370	375	380
Tyr	Leu	Met	Arg	Gln	His	Thr	Asp	Leu	Ser	Leu	Pro	Arg	Ile	Gly	Glu	385	390	395
Ala	Phe	Gly	Gly	Lys	Asp	His	Thr	Thr	Val	Met	Tyr	Ser	Cys	Asp	Lys	405	410	415

Ile Thr Gln Leu Gln Gln Lys Asp Trp Glu Thr Ser Gln Thr Leu Thr
420 425 430

Ser Leu Ser His Arg Ile Asn Ile Ala Gly Gln Ala Pro Glu Ser
435 440 445

<210> 98

<211> 446

<212> PRT

<213> Bacillus subtilis

<400> 98

Met Glu Asn Ile Leu Asp Leu Trp Asn Gln Ala Leu Ala Gln Ile Glu
1 5 10 15

Lys Lys Leu Ser Lys Pro Ser Phe Glu Thr Trp Met Lys Ser Thr Lys
20 25 30

Ala His Ser Leu Gln Gly Asp Thr Leu Thr Ile Thr Ala Pro Asn Glu
35 40 45

Phe Ala Arg Asp Trp Leu Glu Ser Arg Tyr Leu His Leu Ile Ala Asp
50 55 60

Thr Ile Tyr Glu Leu Thr Gly Glu Glu Leu Ser Ile Lys Phe Val Ile
65 70 75 80

Pro Gln Asn Gln Asp Val Glu Asp Phe Met Pro Lys Pro Gln Val Lys
85 90 95

Lys Ala Val Lys Glu Asp Thr Ser Asp Phe Pro Gln Asn Met Leu Asn
100 105 110

Pro Lys Tyr Thr Phe Asp Thr Phe Val Ile Gly Ser Gly Asn Arg Phe
115 120 125

Ala His Ala Ala Ser Leu Ala Val Ala Glu Ala Pro Ala Lys Ala Tyr
130 135 140

Asn Pro Leu Phe Ile Tyr Gly Gly Val Gly Leu Gly Lys Thr His Leu
145 150 155 160

Met His Ala Ile Gly His Tyr Val Ile Asp His Asn Pro Ser Ala Lys
165 170 175

Val Val Tyr Leu Ser Ser Glu Lys Phe Thr Asn Glu Phe Ile Asn Ser
180 185 190

Ile	Arg	Asp	Asn	Lys	Ala	Val	Asp	Phe	Arg	Asn	Arg	Tyr	Arg	Asn	Val			
		195								200				205				
Asp	Val	Leu	Leu	Ile	Asp	Asp	Ile	Gln	Phe	Leu	Ala	Gly	Lys	Glu	Gln			
		210					215					220						
Thr	Gln	Glu	Glu	Phe	Phe	His	Thr	Phe	Asn	Thr	Leu	His	Glu	Glu	Ser			
		225				230					235				240			
Lys	Gln	Ile	Val	Ile	Ser	Ser	Asp	Arg	Pro	Pro	Lys	Glu	Ile	Pro	Thr			
				245						250				255				
Leu	Glu	Asp	Arg	Leu	Arg	Ser	Arg	Phe	Glu	Trp	Gly	Leu	Ile	Thr	Asp			
			260						265					270				
Ile	Thr	Pro	Pro	Asp	Leu	Glu	Thr	Arg	Ile	Ala	Ile	Leu	Arg	Lys	Lys			
		275						280						285				
Ala	Lys	Ala	Glu	Gly	Leu	Asp	Ile	Pro	Asn	Glu	Val	Met	Leu	Tyr	Ile			
		290					295					300						
Ala	Asn	Gln	Ile	Asp	Ser	Asn	Ile	Arg	Glu	Leu	Glu	Gly	Ala	Leu	Ile			
		305				310					315				320			
Arg	Val	Val	Ala	Tyr	Ser	Ser	Leu	Ile	Asn	Lys	Asp	Ile	Asn	Ala	Asp			
				325						330				335				
Leu	Ala	Ala	Glu	Ala	Leu	Lys	Asp	Ile	Ile	Pro	Ser	Ser	Lys	Pro	Lys			
			340						345					350				
Val	Ile	Thr	Ile	Lys	Glu	Ile	Gln	Arg	Val	Val	Gly	Gln	Gln	Phe	Asn			
		355						360					365					
Ile	Lys	Leu	Glu	Asp	Phe	Lys	Ala	Lys	Lys	Arg	Thr	Lys	Ser	Val	Ala			
		370					375					380						
Phe	Pro	Arg	Gln	Ile	Ala	Met	Tyr	Leu	Ser	Arg	Glu	Met	Thr	Asp	Ser			
		385				390					395				400			
Ser	Leu	Pro	Lys	Ile	Gly	Glu	Glu	Phe	Gly	Gly	Arg	Asp	His	Thr	Thr			
				405						410				415				
Val	Ile	His	Ala	His	Glu	Lys	Ile	Ser	Lys	Leu	Leu	Ala	Asp	Asp	Glu			
			420						425				430					
Gln	Leu	Gln	Gln	His	Val	Lys	Glu	Ile	Lys	Glu	Gln	Leu	Lys					
		435						440					445					

<210> 99
 <211> 507
 <212> PRT
 <213> Mycobacterium tuberculosis

<400> 99

Met	Thr	Asp	Asp	Pro	Gly	Ser	Gly	Phe	Thr	Thr	Val	Trp	Asn	Ala	Val
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Val	Ser	Glu	Leu	Asn	Gly	Asp	Pro	Lys	Val	Asp	Asp	Gly	Pro	Ser	Ser
		20						25					30		
Asp	Ala	Asn	Leu	Ser	Ala	Pro	Leu	Thr	Pro	Gln	Gln	Arg	Ala	Trp	Leu
		35					40					45			
Asn	Leu	Val	Gln	Pro	Leu	Thr	Ile	Val	Glu	Gly	Phe	Ala	Leu	Leu	Ser
	50					55					60				
Val	Pro	Ser	Ser	Phe	Val	Gln	Asn	Glu	Ile	Glu	Arg	His	Leu	Arg	Ala
65					70					75					80
Pro	Ile	Thr	Asp	Ala	Leu	Ser	Arg	Arg	Leu	Gly	His	Gln	Ile	Gln	Leu
				85					90					95	
Gly	Val	Arg	Ile	Ala	Pro	Pro	Ala	Thr	Asp	Glu	Ala	Asp	Asp	Thr	Thr
			100					105						110	
Val	Pro	Pro	Ser	Glu	Asn	Pro	Ala	Thr	Thr	Ser	Pro	Asp	Thr	Thr	Thr
		115					120					125			
Asp	Asn	Asp	Glu	Ile	Asp	Asp	Ser	Ala	Ala	Ala	Arg	Gly	Asp	Asn	Gln
		130				135					140				
His	Ser	Trp	Pro	Ser	Tyr	Phe	Thr	Glu	Arg	Pro	His	Asn	Thr	Asp	Ser
145					150					155					160
Ala	Thr	Ala	Gly	Val	Thr	Ser	Leu	Asn	Arg	Arg	Tyr	Thr	Phe	Asp	Thr
				165					170					175	
Phe	Val	Ile	Gly	Ala	Ser	Asn	Arg	Phe	Ala	His	Ala	Ala	Ala	Leu	Ala
			180					185					190		
Ile	Ala	Glu	Ala	Pro	Ala	Arg	Ala	Tyr	Asn	Pro	Leu	Phe	Ile	Trp	Gly
		195					200					205			
Glu	Ser	Gly	Leu	Gly	Lys	Thr	His	Leu	Leu	His	Ala	Ala	Gly	Asn	Tyr

210		215		220
Ala Gln Arg Leu Phe Pro Gly Met Arg Val Lys Tyr Val Ser Thr Glu				
225		230		235 240
Glu Phe Thr Asn Asp Phe Ile Asn Ser Leu Arg Asp Asp Arg Lys Val				
	245		250	255
Ala Phe Lys Arg Ser Tyr Arg Asp Val Asp Val Leu Leu Val Asp Asp				
	260		265	270
Ile Gln Phe Ile Glu Gly Lys Glu Gly Ile Gln Glu Glu Phe Phe His				
	275		280	285
Thr Phe Asn Thr Leu His Asn Ala Asn Lys Gln Ile Val Ile Ser Ser				
	290		295	300
Asp Arg Pro Pro Lys Gln Leu Ala Thr Leu Glu Asp Arg Leu Arg Thr				
305		310		315 320
Arg Phe Glu Trp Gly Leu Ile Thr Asp Val Gln Pro Pro Glu Leu Glu				
	325		330	335
Thr Arg Ile Ala Ile Leu Arg Lys Lys Ala Gln Met Glu Arg Leu Ala				
	340		345	350
Val Pro Asp Asp Val Leu Glu Leu Ile Ala Ser Ser Ile Glu Arg Asn				
	355		360	365
Ile Arg Glu Leu Glu Gly Ala Leu Ile Arg Val Thr Ala Phe Ala Ser				
	370		375	380
Leu Asn Lys Thr Pro Ile Asp Lys Ala Leu Ala Glu Ile Val Leu Arg				
385		390		395 400
Asp Leu Ile Ala Asp Ala Asn Thr Met Gln Ile Ser Ala Ala Thr Ile				
	405		410	415
Met Ala Ala Thr Ala Glu Tyr Phe Asp Thr Thr Val Glu Glu Leu Arg				
	420		425	430
Gly Pro Gly Lys Thr Arg Ala Leu Ala Gln Ser Arg Gln Ile Ala Met				
	435		440	445
Tyr Leu Cys Arg Glu Leu Thr Asp Leu Ser Leu Pro Lys Ile Gly Gln				
	450		455	460
Ala Phe Gly Arg Asp His Thr Thr Val Met Tyr Ala Gln Arg Lys Ile				

465		470		475		480
Leu Ser Glu Met	Ala Glu Arg Arg Glu Val	Phe Asp His Val	Lys Glu			
	485		490		495	
Leu Thr Thr Arg Ile Arg Gln Arg Ser Lys Arg						
	500		505			
<210> 100						
<211> 446						
<212> PRT						
<213> Thermus thermophilus						
<400> 100						
Met Ser His Glu Ala Val Trp Gln His Val Leu Glu His Ile Arg Arg						
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Ser Ile Thr Glu Val Glu Phe His Thr Trp Phe Glu Arg Ile Arg Pro						
	20		25		30	
Leu Gly Ile Arg Asp Gly Val Leu Glu Leu Ala Val Pro Thr Ser Phe						
	35		40		45	
Ala Leu Asp Trp Ile Arg Arg His Tyr Ala Gly Leu Ile Gln Glu Gly						
	50		55		60	
Pro Arg Leu Leu Gly Ala Gln Ala Pro Arg Phe Glu Leu Arg Val Val						
	65		70		75	80
Pro Gly Val Val Val Gln Glu Asp Ile Phe Gln Pro Pro Pro Ser Pro						
	85		90		95	
Pro Ala Gln Ala Gln Pro Glu Asp Thr Phe Lys Thr Ser Trp Trp Gly						
	100		105		110	
Pro Thr Thr Pro Trp Pro His Gly Gly Ala Val Ala Val Ala Glu Ser						
	115		120		125	
Pro Gly Arg Ala Tyr Asn Pro Leu Phe Ile Tyr Gly Gly Arg Gly Leu						
	130		135		140	
Gly Lys Thr Tyr Leu Met His Ala Val Gly Pro Leu Arg Ala Lys Arg						
	145		150		155	160
Phe Pro His Met Arg Leu Glu Tyr Val Ser Thr Glu Thr Phe Thr Asn						
	165		170		175	

Glu	Leu	Ile	Asn	Arg	Pro	Ser	Ala	Arg	Asp	Arg	Met	Thr	Glu	Phe	Arg	180	185	190	
Glu	Arg	Tyr	Arg	Ser	Val	Asp	Leu	Leu	Leu	Val	Asp	Asp	Val	Gln	Phe	195	200	205	
Ile	Ala	Gly	Lys	Glu	Arg	Thr	Gln	Glu	Glu	Phe	Phe	His	Thr	Phe	Asn	210	215	220	
Ala	Leu	Tyr	Glu	Ala	His	Lys	Gln	Ile	Ile	Leu	Ser	Ser	Asp	Arg	Pro	225	230	235	240
Pro	Lys	Asp	Ile	Leu	Thr	Leu	Glu	Ala	Arg	Leu	Arg	Ser	Arg	Phe	Glu	245	250	255	
Trp	Gly	Leu	Ile	Thr	Asp	Asn	Pro	Ala	Pro	Asp	Leu	Glu	Thr	Arg	Ile	260	265	270	
Ala	Ile	Leu	Lys	Met	Asn	Ala	Ser	Ser	Gly	Pro	Glu	Asp	Pro	Glu	Asp	275	280	285	
Ala	Leu	Glu	Tyr	Ile	Ala	Arg	Gln	Val	Thr	Ser	Asn	Ile	Arg	Glu	Trp	290	295	300	
Glu	Gly	Ala	Leu	Met	Arg	Ala	Ser	Pro	Phe	Ala	Ser	Leu	Asn	Gly	Val	305	310	315	320
Glu	Leu	Thr	Arg	Ala	Val	Ala	Ala	Lys	Ala	Leu	Arg	His	Leu	Arg	Pro	325	330	335	
Arg	Glu	Leu	Glu	Ala	Asp	Pro	Leu	Glu	Ile	Ile	Arg	Lys	Ala	Ala	Gly	340	345	350	
Pro	Val	Arg	Pro	Glu	Thr	Pro	Gly	Gly	Ala	His	Gly	Glu	Arg	Arg	Lys	355	360	365	
Lys	Glu	Val	Val	Leu	Pro	Arg	Gln	Leu	Ala	Met	Tyr	Leu	Val	Arg	Glu	370	375	380	
Leu	Thr	Pro	Ala	Ser	Leu	Pro	Glu	Ile	Gly	Gln	Leu	Phe	Gly	Gly	Arg	385	390	395	400
Asp	His	Thr	Thr	Val	Arg	Tyr	Ala	Ile	Gln	Lys	Val	Gln	Glu	Leu	Ala	405	410	415	
Gly	Lys	Pro	Asp	Arg	Glu	Val	Gln	Gly	Leu	Leu	Arg	Thr	Leu	Arg	Glu	420	425	430	

Ala Cys Thr Asp Pro Val Asp Asn Leu Trp Ile Thr Cys Gly
 435 440 445

<210> 101
 <211> 467
 <212> PRT
 <213> Escherichia coli

<400> 101

Met Ser Leu Ser Leu Trp Gln Gln Cys Leu Ala Arg Leu Gln Asp Glu
 1 5 10 15

Leu Pro Ala Thr Glu Phe Ser Met Trp Ile Arg Pro Leu Gln Ala Glu
 20 25 30

Leu Ser Asp Asn Thr Leu Ala Leu Tyr Ala Pro Asn Arg Phe Val Leu
 35 40 45

Asp Trp Val Arg Asp Lys Tyr Leu Asn Asn Ile Asn Gly Leu Leu Thr
 50 55 60

Ser Phe Cys Gly Ala Asp Ala Pro Gln Leu Arg Phe Glu Val Gly Thr
 65 70 75 80

Lys Pro Val Thr Gln Thr Pro Gln Ala Ala Val Thr Ser Asn Val Ala
 85 90 95

Ala Pro Ala Gln Val Ala Gln Thr Gln Pro Gln Arg Ala Ala Pro Ser
 100 105 110

Thr Arg Ser Gly Trp Asp Asn Val Pro Ala Pro Ala Glu Pro Thr Tyr
 115 120 125

Arg Ser Asn Val Asn Val Lys His Thr Phe Asp Asn Phe Val Glu Gly
 130 135 140

Lys Ser Asn Gln Leu Ala Arg Ala Ala Arg Gln Val Ala Asp Asn
 145 150 155 160

Pro Gly Gly Ala Tyr Asn Pro Leu Phe Leu Tyr Gly Gly Thr Gly Leu
 165 170 175

Gly Lys Thr His Leu Leu His Ala Val Gly Asn Gly Ile Met Ala Arg
 180 185 190

Lys Pro Asn Ala Lys Val Val Tyr Met His Ser Glu Arg Phe Val Gln
 195 200 205

Asp	Met	Val	Lys	Ala	Leu	Gln	Asn	Asn	Ala	Ile	Glu	Glu	Phe	Lys	Arg	210	215	220	
Tyr	Tyr	Arg	Ser	Val	Asp	Ala	Leu	Leu	Ile	Asp	Asp	Ile	Gln	Phe	Phe	225	230	235	240
Ala	Asn	Lys	Glu	Arg	Ser	Gln	Glu	Glu	Phe	Phe	His	Thr	Phe	Asn	Ala	245	250	255	
Leu	Leu	Glu	Gly	Asn	Gln	Gln	Ile	Ile	Leu	Thr	Ser	Asp	Arg	Tyr	Pro	260	265	270	
Lys	Glu	Ile	Asn	Gly	Val	Glu	Asp	Arg	Leu	Lys	Ser	Arg	Phe	Gly	Trp	275	280	285	
Gly	Leu	Thr	Val	Ala	Ile	Glu	Pro	Pro	Glu	Leu	Glu	Thr	Arg	Val	Ala	290	295	300	
Ile	Leu	Met	Lys	Lys	Ala	Asp	Glu	Asn	Asp	Ile	Arg	Leu	Pro	Gly	Glu	305	310	315	320
Val	Ala	Phe	Phe	Ile	Ala	Lys	Arg	Leu	Arg	Ser	Asn	Val	Arg	Glu	Leu	325	330	335	
Glu	Gly	Ala	Leu	Asn	Arg	Val	Ile	Ala	Asn	Ala	Asn	Phe	Thr	Gly	Arg	340	345	350	
Ala	Ile	Thr	Ile	Asp	Phe	Val	Arg	Glu	Ala	Leu	Arg	Asp	Leu	Leu	Ala	355	360	365	
Leu	Gln	Glu	Lys	Leu	Val	Thr	Ile	Asp	Asn	Ile	Gln	Lys	Thr	Val	Ala	370	375	380	
Glu	Tyr	Tyr	Lys	Ile	Lys	Val	Ala	Asp	Leu	Leu	Ser	Lys	Arg	Arg	Ser	385	390	395	400
Arg	Ser	Val	Ala	Arg	Pro	Arg	Gln	Met	Ala	Met	Ala	Leu	Ala	Lys	Glu	405	410	415	
Leu	Thr	Asn	His	Ser	Leu	Pro	Glu	Ile	Gly	Asp	Ala	Phe	Gly	Gly	Arg	420	425	430	
Asp	His	Thr	Thr	Val	Leu	His	Ala	Cys	Arg	Lys	Ile	Glu	Gln	Leu	Arg	435	440	445	
Glu	Glu	Ser	His	Asp	Ile	Lys	Glu	Asp	Phe	Ser	Asn	Leu	Ile	Arg	Thr	450	455	460	

Leu Ser Ser
465

<210> 102
<211> 440
<212> PRT
<213> *Thermatoga maritima*

<400> 102
Met Lys Glu Arg Ile Leu Gln Glu Ile Lys Thr Arg Val Asn Arg Lys
1 5 10 15
Ser Trp Glu Leu Trp Phe Ser Ser Phe Asp Val Lys Ser Ile Glu Gly
20 25 30
Asn Lys Val Val Phe Ser Val Gly Asn Leu Phe Ile Lys Glu Trp Leu
35 40 45
Glu Lys Lys Tyr Tyr Ser Val Leu Ser Lys Ala Val Lys Val Val Leu
50 55 60
Gly Asn Asp Ala Thr Phe Glu Ile Thr Tyr Glu Ala Phe Glu Pro His
65 70 75 80
Ser Ser Tyr Ser Glu Pro Leu Val Lys Lys Arg Ala Val Leu Leu Thr
85 90 95
Pro Leu Asn Pro Asp Tyr Thr Phe Glu Asn Phe Val Val Gly Pro Gly
100 105 110
Asn Ser Phe Ala Tyr His Ala Ala Leu Glu Val Ala Lys His Pro Gly
115 120 125
Arg Tyr Asn Pro Leu Phe Ile Tyr Gly Gly Val Gly Leu Gly Lys Thr
130 135 140
His Leu Leu Gln Ser Ile Gly Asn Tyr Val Val Gln Asn Glu Pro Asp
145 150 155 160
Leu Arg Val Met Tyr Ile Thr Ser Glu Lys Phe Leu Asn Asp Leu Val
165 170 175
Asp Ser Met Lys Glu Gly Lys Leu Asn Glu Phe Arg Glu Lys Tyr Arg
180 185 190
Lys Lys Val Asp Ile Leu Leu Ile Asp Asp Val Gln Phe Leu Ile Gly

195	200	205
Lys Thr Gly Val Gln Thr Glu Leu Phe His Thr Phe Asn Glu Leu His		
210	215	220
Asp Ser Gly Lys Gln Ile Val Ile Cys Ser Asp Arg Glu Pro Gln Lys		
225	230	235 240
Leu Ser Glu Phe Gln Asp Arg Leu Val Ser Arg Phe Gln Met Gly Leu		
	245	250 255
Val Ala Lys Leu Glu Pro Pro Asp Glu Glu Thr Arg Lys Ser Ile Ala		
	260	265 270
Arg Lys Met Leu Glu Ile Glu His Gly Glu Leu Pro Glu Glu Val Leu		
	275	280 285
Asn Phe Val Ala Glu Asn Val Asp Asp Asn Leu Arg Arg Leu Arg Gly		
	290	295 300
Ala Ile Ile Lys Leu Leu Val Tyr Lys Glu Thr Thr Gly Lys Glu Val		
305	310	315 320
Asp Leu Lys Glu Ala Ile Leu Leu Leu Lys Asp Phe Ile Lys Pro Asn		
	325	330 335
Arg Val Lys Ala Met Asp Pro Ile Asp Glu Leu Ile Glu Ile Val Ala		
	340	345 350
Lys Val Thr Gly Val Pro Arg Glu Glu Ile Leu Ser Asn Ser Arg Asn		
	355	360 365
Val Lys Ala Leu Thr Ala Arg Arg Ile Gly Met Tyr Val Ala Lys Asn		
	370	375 380
Tyr Leu Lys Ser Ser Leu Arg Thr Ile Ala Glu Lys Phe Asn Arg Ser		
385	390	395 400
His Pro Val Val Val Asp Ser Val Lys Lys Val Lys Asp Ser Leu Leu		
	405	410 415
Lys Gly Asn Lys Gln Leu Lys Ala Leu Ile Asp Glu Val Ile Gly Glu		
	420	425 430
Ile Ser Arg Arg Ala Leu Ser Gly		
	435	440

<210> 103
 <211> 457
 <212> PRT
 <213> Helicobacter pylori

<400> 103

Met Asp Thr Asn Asn Asn Ile Glu Lys Glu Ile Leu Ala Leu Val Lys
 1 5 10 15

Gln Asn Pro Lys Val Ser Leu Ile Glu Tyr Glu Asn Tyr Phe Ser Gln
 20 25 30

Leu Lys Tyr Asn Pro Asn Ala Ser Lys Ser Asp Ile Ala Phe Phe Tyr
 35 40 45

Ala Pro Asn Gln Val Leu Cys Thr Thr Ile Thr Ala Lys Tyr Gly Ala
 50 55 60

Leu Leu Lys Glu Ile Leu Ser Gln Asn Lys Val Gly Met His Leu Ala
 65 70 75 80

His Ser Val Asp Val Arg Ile Glu Val Ala Pro Lys Ile Gln Ile Asn
 85 90 95

Ala Gln Ser Asn Ile Asn Tyr Lys Ala Ile Lys Thr Ser Val Lys Asp
 100 105 110

Ser Tyr Thr Phe Glu Asn Phe Val Val Gly Ser Cys Asn Asn Thr Val
 115 120 125

Tyr Glu Ile Ala Lys Lys Val Ala Gln Ser Asp Thr Pro Pro Tyr Asn
 130 135 140

Pro Val Leu Phe Tyr Gly Gly Thr Gly Leu Gly Lys Thr His Ile Leu
 145 150 155 160

Asn Ala Ile Gly Asn His Ala Leu Glu Lys His Lys Lys Val Val Leu
 165 170 175

Val Thr Ser Glu Asp Phe Leu Thr Asp Phe Leu Lys His Leu Asp Asn
 180 185 190

Lys Thr Met Asp Ser Phe Lys Ala Lys Tyr Arg His Cys Asp Phe Phe
 195 200 205

Leu Leu Asp Asp Ala Gln Phe Leu Gln Gly Lys Pro Lys Leu Glu Glu
 210 215 220

Glu Phe Phe His Thr Phe Asn Glu Leu His Ala Asn Ser Lys Gln Ile
 225 230 235 240

Val Leu Ile Ser Asp Arg Ser Pro Lys Asn Ile Ala Gly Leu Glu Asp
 245 250 255

Arg Leu Lys Ser Arg Phe Glu Trp Gly Ile Thr Ala Lys Val Met Pro
 260 265 270

Pro Asp Leu Glu Thr Lys Leu Ser Ile Val Lys Gln Lys Cys Gln Leu
 275 280 285

Asn Gln Ile Thr Leu Pro Glu Glu Val Met Glu Tyr Ile Ala Gln His
 290 295 300

Ile Ser Asp Asn Ile Arg Gln Met Glu Gly Ala Ile Ile Lys Ile Ser
 305 310 315 320

Val Asn Ala Asn Leu Met Asn Ala Ser Ile Asp Leu Asn Leu Ala Lys
 325 330 335

Thr Val Leu Glu Asp Leu Gln Lys Asp His Ala Glu Gly Ser Ser Leu
 340 345 350

Glu Asn Ile Leu Leu Ala Val Ala Gln Ser Leu Asn Leu Lys Ser Ser
 355 360 365

Glu Ile Lys Val Ser Ser Arg Gln Lys Asn Val Ala Leu Ala Arg Lys
 370 375 380

Leu Val Val Tyr Phe Ala Arg Leu Tyr Thr Pro Asn Pro Thr Leu Ser
 385 390 395 400

Leu Ala Gln Phe Leu Asp Leu Lys Asp His Ser Ser Ile Ser Lys Met
 405 410 415

Tyr Ser Gly Val Lys Lys Met Leu Glu Glu Glu Lys Ser Pro Phe Val
 420 425 430

Leu Ser Leu Arg Glu Glu Ile Lys Asn Arg Leu Asn Glu Leu Asn Asp
 435 440 445

Lys Lys Thr Ala Phe Asn Ser Ser Glu
 450 455

<210> 104

<211> 1305

<212> DNA

<213> *Thermus thermophilus*

<400> 104

```
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gagctcgccg tgcccacctc ctttgccctg gactggatcc ggcgccacta cgccggcctc 180
atccaggagg gccctcggct cctcggggcc caggcgcccc ggtttgagct ccgggtggtg 240
cccggggtcg tagtccagga ggacatcttc cagccccccg cgagcccccc ggcccaagct 300
caacccgaag atacctttaa aacttcgtgg tggggcccaa caactccatg gccccacggc 360
ggcgccgtgg cagtggccga gtcccccggc cgggcctaca accccctctt catctacggg 420
ggcgtggcc tgggaaagac ctacctgatg cacgccgtgg gccactccg tgcgaagcgc 480
ttccccaca tgagattaga gtacgtttcc acggaaactt tcaccaacga gctcatcaac 540
cggccatccg cgagggaccg gatgacggag ttccgggagc ggtaccgctc cgtggacctc 600
ctgctggtgg acgacgtcca gttcatcgcc ggaaaggagc gcaccagga ggagtttttc 660
cacaccttca acgcccttta cgaggccac aagcagatca tcctctctc cgaccggcgc 720
cccaaggaca tcctcacctt ggaggcgcgc ctgcggagcc gctttgagtg gggcctgata 780
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ggagctcacg gggagcgccg caagaaggag gtggtcctcc cccggcagct cgccatgtac 1140
ctggtgctgg agctcacccc ggccctccctg cccgagatcg accagctcaa cgacgaccgg 1200
gaccacacca cggctcctta cgccatccag aaggtccagg agctcgcgga aagcgaccgg 1260
gaggtgcagg gcctcctccg caccctccgg gaggcgtgca catga 1305
```

<210> 105

<211> 434

<212> PRT

<213> *Thermus thermophilus*

<400> 105

```
Val Ser His Glu Ala Val Trp Gln His Val Leu Glu His Ile Arg Arg
  1              5              10              15
```

```
Ser Ile Thr Glu Val Glu Phe His Thr Trp Phe Glu Arg Ile Arg Pro
          20              25              30
```

```
Leu Gly Ile Arg Asp Gly Val Leu Glu Leu Ala Val Pro Thr Ser Phe
      35              40              45
```

```
Ala Leu Asp Trp Ile Arg Arg His Tyr Ala Gly Leu Ile Gln Glu Gly
      50              55              60
```

```
Pro Arg Leu Leu Gly Ala Gln Ala Pro Arg Phe Glu Leu Arg Val Val
      65              70              75              80
```

Pro Gly Val Val Val Gln Glu Asp Ile Phe Gln Pro Pro Pro Ser Pro
 85 90 95

Pro Ala Gln Ala Gln Pro Glu Asp Thr Phe Lys Thr Ser Trp Trp Gly
 100 105 110

Pro Thr Thr Pro Trp Pro His Gly Gly Ala Val Ala Val Ala Glu Ser
 115 120 125

Pro Gly Arg Ala Tyr Asn Pro Leu Phe Ile Tyr Gly Gly Arg Gly Leu
 130 135 140

Gly Lys Thr Tyr Leu Met His Ala Val Gly Pro Leu Arg Ala Lys Arg
 145 150 155 160

Phe Pro His Met Arg Leu Glu Tyr Val Ser Thr Glu Thr Phe Thr Asn
 165 170 175

Glu Leu Ile Asn Arg Pro Ser Ala Arg Asp Arg Met Thr Glu Phe Arg
 180 185 190

Glu Arg Tyr Arg Ser Val Asp Leu Leu Leu Val Asp Asp Val Gln Phe
 195 200 205

Ile Ala Gly Lys Glu Arg Thr Gln Glu Glu Phe Phe His Thr Phe Asn
 210 215 220

Ala Leu Tyr Glu Ala His Lys Gln Ile Ile Leu Ser Ser Asp Arg Pro
 225 230 235 240

Pro Lys Asp Ile Leu Thr Leu Glu Ala Arg Leu Arg Ser Arg Phe Glu
 245 250 255

Trp Gly Leu Ile Thr Asp Asn Pro Ala Pro Asp Leu Glu Thr Arg Ile
 260 265 270

Ala Ile Leu Lys Met Asn Ala Ser Ser Gly Pro Glu Asp Pro Glu Asp
 275 280 285

Ala Leu Glu Tyr Ile Ala Arg Gln Val Thr Ser Asn Ile Arg Glu Trp
 290 295 300

Glu Gly Ala Leu Met Arg Ala Ser Pro Phe Ala Ser Leu Asn Gly Val
 305 310 315 320

Glu Leu Thr Arg Ala Val Ala Ala Lys Ala Leu Arg His Leu Arg Pro
 325 330 335

Arg Glu Leu Glu Ala Asp Pro Leu Glu Ile Ile Arg Lys Ala Ala Gly
 340 345 350

Pro Val Arg Pro Glu Thr Pro Gly Gly Ala His Gly Glu Arg Arg Lys
 355 360 365

Lys Glu Val Val Leu Pro Arg Gln Leu Ala Met Tyr Leu Val Arg Glu
 370 375 380

Leu Thr Pro Ala Ser Leu Pro Glu Ile Asp Gln Leu Asn Asp Asp Arg
 385 390 395 400

Asp His Thr Thr Val Leu Tyr Ala Ile Gln Lys Val Gln Glu Leu Ala
 405 410 415

Glu Ser Asp Arg Glu Val Gln Gly Leu Leu Arg Thr Leu Arg Glu Ala
 420 425 430

Cys Thr

<210> 106

<211> 1128

<212> DNA

<213> *Thermus thermophilus*

<400> 106

```

atgaacataa cggttcccaa aaaactcctc tcggaccagc tttccctcct ggagcgcac 60
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gccttgatcc tcttcgggac caacggggag gtggacctcg aggtccgcct ccccgccgag 180
gccccaaagcc tccccgggt gctcgtcccc gccagccct tcttcagct ggtgcgagc 240
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gagctctcct ccgggcgttt ccgcaccgg ctcagcctgg cccctgccga gggctacccc 360
gagcttctgg tgcccgagg ggaggacaag ggggccttcc cctcggac gcgatgccc 420
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cgggccatct tccgcggggt gcagctggag ttctcccccc agggcttcg ggcggtggcc 540
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cccggtgggg accgggcca cctgggcac tccgggcca cgagcccgag cctcatctgg 1080
ggggacgggg aggggtacc ggcggtggtg gtgccctca ggtctag 1128

```

<210> 107

<211> 376

<212> PRT

<213> Thermus thermophilus

<400> 107

Met Asn Ile Thr Val Pro Lys Lys Leu Leu Ser Asp Gln Leu Ser Leu
1 5 10 15

Leu Glu Arg Ile Val Pro Ser Arg Ser Ala Asn Pro Leu Tyr Thr Tyr
20 25 30

Leu Gly Leu Tyr Ala Glu Glu Gly Ala Leu Ile Leu Phe Gly Thr Asn
35 40 45

Gly Glu Val Asp Leu Glu Val Arg Leu Pro Ala Glu Ala Gln Ser Leu
50 55 60

Pro Arg Val Leu Val Pro Ala Gln Pro Phe Phe Gln Leu Val Arg Ser
65 70 75 80

Leu Pro Gly Asp Leu Val Ala Leu Gly Leu Ala Ser Glu Pro Gly Gln
85 90 95

Gly Gly Gln Leu Glu Leu Ser Ser Gly Arg Phe Arg Thr Arg Leu Ser
100 105 110

Leu Ala Pro Ala Glu Gly Tyr Pro Glu Leu Leu Val Pro Glu Gly Glu
115 120 125

Asp Lys Gly Ala Phe Pro Leu Arg Thr Arg Met Pro Ser Gly Glu Leu
130 135 140

Val Lys Ala Leu Thr His Val Arg Tyr Ala Ala Ser Asn Glu Glu Tyr
145 150 155 160

Arg Ala Ile Phe Arg Gly Val Gln Leu Glu Phe Ser Pro Gln Gly Phe
165 170 175

Arg Ala Val Ala Ser Asp Gly Tyr Arg Leu Ala Leu Tyr Asp Leu Pro
180 185 190

Leu Pro Gln Gly Phe Gln Ala Lys Ala Val Val Pro Ala Arg Ser Val
195 200 205

Asp Glu Met Val Arg Val Leu Lys Gly Ala Asp Gly Ala Glu Ala Val

210		215		220
Leu Ala Leu Gly Glu Gly Val Leu Ala Leu Ala Leu Glu Gly Gly Ser				
225		230		235 240
Gly Val Arg Met Ala Leu Arg Leu Met Glu Gly Glu Phe Pro Asp Tyr				
	245		250	255
Gln Arg Val Ile Pro Gln Glu Phe Ala Leu Lys Val Gln Val Glu Gly				
	260		265	270
Glu Ala Leu Arg Glu Ala Val Arg Arg Val Ser Val Leu Ser Asp Arg				
	275		280	285
Gln Asn His Arg Val Asp Leu Leu Leu Glu Glu Gly Arg Ile Leu Leu				
	290		295	300
Ser Ala Glu Gly Asp Tyr Gly Lys Gly Gln Glu Glu Val Pro Ala Gln				
305		310		315 320
Val Glu Gly Pro Asp Met Ala Val Ala Tyr Asn Ala Arg Tyr Leu Leu				
	325		330	335
Glu Ala Leu Ala Pro Val Gly Asp Arg Ala His Leu Gly Ile Ser Gly				
	340		345	350
Pro Thr Ser Pro Ser Leu Ile Trp Gly Asp Gly Glu Gly Tyr Arg Ala				
	355		360	365
Val Val Val Pro Leu Arg Val Glx				
	370		375	

<210> 108

<211> 376

<212> PRT

<213> Thermus thermophilus

<400> 108

Met Asn Ile Thr Val Pro Lys Lys Leu Leu Ser Asp Gln Leu Ser Leu
1 5 10 15
Leu Glu Arg Ile Val Pro Ser Arg Ser Ala Asn Pro Leu Tyr Thr Tyr
20 25 30
Leu Gly Leu Tyr Ala Glu Glu Gly Ala Leu Ile Leu Phe Gly Thr Asn
35 40 45

Gly	Glu	Val	Asp	Leu	Glu	Val	Arg	Leu	Pro	Ala	Glu	Ala	Gln	Ser	Leu	50	55	60	
Pro	Arg	Val	Leu	Val	Pro	Ala	Gln	Pro	Phe	Phe	Gln	Leu	Val	Arg	Ser	65	70	75	80
Leu	Pro	Gly	Asp	Leu	Val	Ala	Leu	Gly	Leu	Ala	Ser	Glu	Pro	Gly	Gln	85	90	95	
Gly	Gly	Gln	Leu	Glu	Leu	Ser	Ser	Gly	Arg	Phe	Arg	Thr	Arg	Leu	Ser	100	105	110	
Leu	Ala	Pro	Ala	Glu	Gly	Tyr	Pro	Glu	Leu	Leu	Val	Pro	Glu	Gly	Glu	115	120	125	
Asp	Lys	Gly	Ala	Phe	Pro	Leu	Arg	Thr	Arg	Met	Pro	Ser	Gly	Glu	Leu	130	135	140	
Val	Lys	Ala	Leu	Thr	His	Val	Arg	Tyr	Ala	Ala	Ser	Asn	Glu	Glu	Tyr	145	150	155	160
Arg	Ala	Ile	Phe	Arg	Gly	Val	Gln	Leu	Glu	Phe	Ser	Pro	Gln	Gly	Phe	165	170	175	
Arg	Ala	Val	Ala	Ser	Asp	Gly	Tyr	Arg	Leu	Ala	Leu	Tyr	Asp	Leu	Pro	180	185	190	
Leu	Pro	Gln	Gly	Phe	Gln	Ala	Lys	Ala	Val	Val	Pro	Ala	Arg	Ser	Val	195	200	205	
Asp	Glu	Met	Val	Arg	Val	Leu	Lys	Gly	Ala	Asp	Gly	Ala	Glu	Ala	Val	210	215	220	
Leu	Ala	Leu	Gly	Glu	Gly	Val	Leu	Ala	Leu	Ala	Leu	Glu	Gly	Gly	Ser	225	230	235	240
Gly	Val	Arg	Met	Ala	Leu	Arg	Leu	Met	Glu	Gly	Glu	Phe	Pro	Asp	Tyr	245	250	255	
Gln	Arg	Val	Ile	Pro	Gln	Glu	Phe	Ala	Leu	Lys	Val	Gln	Val	Glu	Gly	260	265	270	
Glu	Ala	Leu	Arg	Glu	Ala	Val	Arg	Arg	Val	Ser	Val	Leu	Ser	Asp	Arg	275	280	285	
Gln	Asn	His	Arg	Val	Asp	Leu	Leu	Leu	Glu	Glu	Gly	Arg	Ile	Leu	Leu	290	295	300	

Ser Ala Glu Gly Asp Tyr Gly Lys Gly Gln Glu Glu Val Pro Ala Gln
 305 310 315 320

Val Glu Gly Pro Asp Met Ala Val Ala Tyr Asn Ala Arg Tyr Leu Leu
 325 330 335

Glu Ala Leu Ala Pro Val Gly Asp Arg Ala His Leu Gly Ile Ser Gly
 340 345 350

Pro Thr Ser Pro Ser Leu Ile Trp Gly Asp Gly Glu Gly Tyr Arg Ala
 355 360 365

Val Val Val Pro Leu Arg Val Glx
 370 375

<210> 109

<211> 367

<212> PRT

<213> Escherichia coli

<400> 109

Met Lys Phe Thr Val Glu Arg Glu His Leu Leu Lys Pro Leu Gln Gln
 1 5 10 15

Val Ser Gly Pro Leu Gly Gly Arg Pro Thr Leu Pro Ile Leu Gly Asn
 20 25 30

Leu Leu Leu Gln Val Ala Asp Gly Thr Leu Ser Leu Thr Gly Thr Asp
 35 40 45

Leu Glu Met Glu Met Val Ala Arg Val Ala Leu Val Gln Pro His Glu
 50 55 60

Pro Gly Ala Thr Thr Val Pro Ala Arg Lys Phe Phe Asp Ile Cys Arg
 65 70 75 80

Gly Leu Pro Glu Gly Ala Glu Ile Ala Val Gln Leu Glu Gly Glu Arg
 85 90 95

Met Leu Val Arg Ser Gly Arg Ser Arg Phe Ser Leu Ser Thr Leu Pro
 100 105 110

Ala Ala Asp Phe Pro Asn Leu Asp Asp Trp Gln Ser Glu Val Glu Phe
 115 120 125

Thr Leu Pro Gln Ala Thr Met Lys Arg Leu Ile Glu Ala Thr Gln Phe
 130 135 140

Ser	Met	Ala	His	Gln	Asp	Val	Arg	Tyr	Tyr	Leu	Asn	Gly	Met	Leu	Phe	145	150	155	160
Glu	Thr	Glu	Gly	Glu	Glu	Leu	Arg	Thr	Val	Ala	Thr	Asp	Gly	His	Arg	165	170	175	
Leu	Ala	Val	Cys	Ser	Met	Pro	Ile	Gly	Gln	Ser	Leu	Pro	Ser	His	Ser	180	185	190	
Val	Ile	Val	Pro	Arg	Lys	Gly	Val	Ile	Glu	Leu	Met	Arg	Met	Leu	Asp	195	200	205	
Gly	Gly	Asp	Asn	Pro	Leu	Arg	Val	Gln	Ile	Gly	Ser	Asn	Asn	Ile	Arg	210	215	220	
Ala	His	Val	Gly	Asp	Phe	Ile	Phe	Thr	Ser	Lys	Leu	Val	Asp	Gly	Arg	225	230	235	240
Phe	Pro	Asp	Tyr	Arg	Arg	Val	Leu	Pro	Lys	Asn	Pro	Asp	Lys	His	Leu	245	250	255	
Glu	Ala	Gly	Cys	Asp	Leu	Leu	Lys	Gln	Ala	Phe	Ala	Arg	Ala	Ala	Ile	260	265	270	
Leu	Ser	Asn	Glu	Lys	Phe	Arg	Gly	Val	Arg	Leu	Tyr	Val	Ser	Glu	Asn	275	280	285	
Gln	Leu	Lys	Ile	Thr	Ala	Asn	Asn	Pro	Glu	Gln	Glu	Glu	Ala	Glu	Glu	290	295	300	
Ile	Leu	Asp	Val	Thr	Tyr	Ser	Gly	Ala	Glu	Met	Glu	Ile	Gly	Phe	Asn	305	310	315	320
Val	Ser	Tyr	Val	Leu	Asp	Val	Leu	Asn	Ala	Leu	Lys	Cys	Glu	Asn	Val	325	330	335	
Arg	Met	Met	Leu	Thr	Asp	Ser	Val	Ser	Ser	Val	Gln	Ile	Glu	Asp	Ala	340	345	350	
Ala	Ser	Gln	Ser	Ala	Ala	Tyr	Val	Val	Met	Pro	Met	Arg	Leu	Glx	355	360	365		

<210> 110

<211> 367

<212> PRT

<213> Proteus mirabilis

<400> 110

Met Lys Phe Ile Ile Glu Arg Glu Gln Leu Leu Lys Pro Leu Gln Gln
1 5 10 15

Val Ser Gly Pro Leu Gly Gly Arg Pro Thr Leu Pro Ile Leu Gly Asn
20 25 30

Leu Leu Leu Lys Val Thr Glu Asn Thr Leu Ser Leu Thr Gly Thr Asp
35 40 45

Leu Glu Met Glu Met Met Ala Arg Val Ser Leu Ser Gln Ser His Glu
50 55 60

Ile Gly Ala Thr Thr Val Pro Ala Arg Lys Phe Phe Asp Ile Trp Arg
65 70 75 80

Gly Leu Pro Glu Gly Ala Glu Ile Ser Val Glu Leu Asp Gly Asp Arg
85 90 95

Leu Leu Val Arg Ser Gly Arg Ser Arg Phe Ser Leu Ser Thr Leu Pro
100 105 110

Ala Ser Asp Phe Pro Asn Leu Asp Asp Trp Gln Ser Glu Val Glu Phe
115 120 125

Thr Leu Pro Gln Ala Thr Leu Lys Arg Leu Ile Glu Ser Thr Gln Phe
130 135 140

Ser Met Ala His Gln Asp Val Arg Tyr Tyr Leu Asn Gly Met Leu Phe
145 150 155 160

Glu Thr Glu Asn Thr Glu Leu Arg Thr Val Ala Thr Asp Gly His Arg
165 170 175

Leu Ala Val Cys Ala Met Asp Ile Gly Gln Ser Leu Pro Gly His Ser
180 185 190

Val Ile Val Pro Arg Lys Gly Val Ile Glu Leu Met Arg Leu Leu Asp
195 200 205

Gly Ser Gly Glu Ser Leu Leu Gln Leu Gln Ile Gly Ser Asn Asn Leu
210 215 220

Arg Ala His Val Gly Asp Phe Ile Phe Thr Ser Lys Leu Val Asp Gly
225 230 235 240

Arg Phe Pro Asp Tyr Arg Arg Val Leu Pro Lys Asn Pro Thr Lys Thr

Ala	Leu	Val	Gln	Ser	Gly	Arg	Ser	Arg	Phe	Thr	Leu	Ala	Thr	Gln	Pro	100	105	110	
Ala	Glu	Glu	Tyr	Pro	Asn	Leu	Thr	Asp	Trp	Gln	Ser	Glu	Val	Asp	Phe	115	120	125	
Glu	Leu	Pro	Gln	Asn	Thr	Leu	Arg	Arg	Leu	Ile	Glu	Ala	Thr	Gln	Phe	130	135	140	
Ser	Met	Ala	Asn	Gln	Asp	Ala	Arg	Tyr	Phe	Leu	Asn	Gly	Met	Lys	Phe	145	150	155	160
Glu	Thr	Glu	Gly	Asn	Leu	Leu	Arg	Thr	Val	Ala	Thr	Asp	Gly	His	Arg	165	170	175	
Leu	Ala	Val	Cys	Thr	Ile	Ser	Leu	Glu	Gln	Glu	Leu	Gln	Asn	His	Ser	180	185	190	
Val	Ile	Leu	Pro	Arg	Lys	Gly	Val	Leu	Glu	Leu	Val	Arg	Leu	Leu	Glu	195	200	205	
Thr	Asn	Asp	Glu	Pro	Ala	Arg	Leu	Gln	Ile	Gly	Thr	Asn	Asn	Leu	Arg	210	215	220	
Val	His	Leu	Lys	Asn	Thr	Val	Phe	Thr	Ser	Lys	Leu	Ile	Asp	Gly	Arg	225	230	235	240
Phe	Pro	Asp	Tyr	Arg	Arg	Val	Leu	Pro	Arg	Asn	Ala	Thr	Lys	Ile	Val	245	250	255	
Glu	Gly	Asn	Trp	Glu	Met	Leu	Lys	Gln	Ala	Phe	Ala	Arg	Ala	Ser	Ile	260	265	270	
Leu	Ser	Asn	Glu	Arg	Ala	Arg	Ser	Val	Arg	Leu	Ser	Leu	Lys	Glu	Asn	275	280	285	
Gln	Leu	Lys	Ile	Thr	Ala	Ser	Asn	Thr	Glu	His	Glu	Glu	Ala	Glu	Glu	290	295	300	
Ile	Val	Asp	Val	Asn	Tyr	Asn	Gly	Glu	Glu	Leu	Glu	Val	Gly	Phe	Asn	305	310	315	320
Val	Thr	Tyr	Ile	Leu	Asp	Val	Leu	Asn	Ala	Leu	Lys	Cys	Asn	Gln	Val	325	330	335	
Arg	Met	Cys	Leu	Thr	Asp	Ala	Phe	Ser	Ser	Cys	Leu	Ile	Glu	Asn	Cys	340	345	350	

Glu Asp Ser Ser Cys Glu Tyr Val Ile Met Pro Met Arg Leu
 355 360 365

<210> 112

<211> 367

<212> PRT

<213> Pseudomonas putida

<400> 112

Met His Phe Thr Ile Gln Arg Glu Ala Leu Leu Lys Pro Leu Gln Leu
 1 5 10 15

Val Ala Gly Val Val Glu Arg Arg Gln Thr Leu Pro Val Leu Ser Asn
 20 25 30

Val Leu Leu Val Val Gln Gly Gln Gln Leu Ser Leu Thr Gly Thr Asp
 35 40 45

Leu Glu Val Glu Leu Val Gly Arg Val Gln Leu Glu Glu Pro Ala Glu
 50 55 60

Pro Gly Glu Ile Thr Val Pro Ala Arg Lys Leu Met Asp Ile Cys Lys
 65 70 75 80

Ser Leu Pro Asn Asp Ala Leu Ile Asp Ile Lys Val Asp Glu Gln Lys
 85 90 95

Leu Leu Val Lys Ala Gly Arg Ser Arg Phe Thr Leu Ser Thr Leu Pro
 100 105 110

Ala Asn Asp Phe Pro Thr Val Glu Glu Gly Pro Gly Ser Leu Thr Cys
 115 120 125

Asn Leu Glu Gln Ser Lys Leu Arg Arg Leu Ile Glu Arg Thr Ser Phe
 130 135 140

Ala Met Ala Gln Gln Asp Val Arg Tyr Tyr Leu Asn Gly Met Leu Leu
 145 150 155 160

Glu Val Ser Arg Asn Thr Leu Arg Ala Val Ser Thr Asp Gly His Arg
 165 170 175

Leu Ala Leu Cys Ser Met Ser Ala Pro Ile Glu Gln Glu Asp Arg His
 180 185 190

Gln Val Ile Val Pro Arg Lys Gly Ile Leu Glu Leu Ala Arg Leu Leu
 195 200 205

Thr Asp Pro Glu Gly Met Val Ser Ile Val Leu Gly Gln His His Ile
 210 215 220

Arg Ala Thr Thr Gly Glu Phe Thr Phe Thr Ser Lys Leu Val Asp Gly
 225 230 235 240

Lys Phe Pro Asp Tyr Glu Arg Val Leu Pro Lys Gly Gly Asp Lys Leu
 245 250 255

Val Val Gly Asp Arg Gln Ala Leu Arg Glu Ala Phe Ser Arg Thr Ala
 260 265 270

Ile Leu Ser Asn Glu Lys Tyr Arg Gly Ile Arg Leu Gln Leu Ala Ala
 275 280 285

Gly Gln Leu Lys Ile Gln Ala Asn Asn Pro Glu Gln Glu Glu Ala Glu
 290 295 300

Glu Glu Ile Ser Val Asp Tyr Glu Gly Ser Ser Leu Glu Ile Gly Phe
 305 310 315 320

Asn Val Ser Tyr Leu Leu Asp Val Leu Gly Val Met Thr Thr Glu Gln
 325 330 335

Val Arg Leu Ile Leu Ser Asp Ser Asn Ser Ser Ala Leu Leu Gln Glu
 340 345 350

Ala Gly Asn Asp Asp Ser Ser Tyr Val Val Met Pro Met Arg Leu
 355 360 365

<210> 113

<211> 366

<212> PRT

<213> Buchnera aphidicola

<400> 113

Met Lys Phe Thr Ile Gln Asn Asp Ile Leu Thr Lys Asn Leu Lys Lys
 1 5 10 15

Ile Thr Arg Val Leu Val Lys Asn Ile Ser Phe Pro Ile Leu Glu Asn
 20 25 30

Ile Leu Ile Gln Val Glu Asp Gly Thr Leu Ser Leu Thr Thr Thr Asn
 35 40 45

Leu Glu Ile Glu Leu Ile Ser Lys Ile Glu Ile Ile Thr Lys Tyr Ile

50		55		60
Pro Gly Lys Thr Thr Ile Ser Gly Arg Lys Ile Leu Asn Ile Cys Arg				
65		70		75
Thr Leu Ser Glu Lys Ser Lys Ile Lys Met Gln Leu Lys Asn Lys Lys				
	85		90	95
Met Tyr Ile Ser Ser Glu Asn Ser Asn Tyr Ile Leu Ser Thr Leu Ser				
	100		105	110
Ala Asp Thr Phe Pro Asn His Gln Asn Phe Asp Tyr Ile Ser Lys Phe				
	115		120	125
Asp Ile Ser Ser Asn Ile Leu Lys Glu Met Ile Glu Lys Thr Glu Phe				
	130		135	140
Ser Met Gly Lys Gln Asp Val Arg Tyr Tyr Leu Asn Gly Met Leu Leu				
145		150		155
Glu Lys Lys Asp Lys Phe Leu Arg Ser Val Ala Thr Asp Gly Tyr Arg				
	165		170	175
Leu Ala Ile Ser Tyr Thr Gln Leu Lys Lys Asp Ile Asn Phe Phe Ser				
	180		185	190
Ile Ile Ile Pro Asn Lys Ala Val Met Glu Leu Leu Lys Leu Leu Asn				
	195		200	205
Thr Gln Pro Gln Leu Leu Asn Ile Leu Ile Gly Ser Asn Ser Ile Arg				
	210		215	220
Ile Tyr Thr Lys Asn Leu Ile Phe Thr Thr Gln Leu Ile Glu Gly Glu				
225		230		235
Tyr Pro Asp Tyr Lys Ser Val Leu Phe Lys Glu Lys Lys Asn Pro Ile				
	245		250	255
Ile Thr Asn Ser Ile Leu Leu Lys Lys Ser Leu Leu Arg Val Ala Ile				
	260		265	270
Leu Ala His Glu Lys Phe Cys Gly Ile Glu Ile Lys Ile Glu Asn Gly				
	275		280	285
Lys Phe Lys Val Leu Ser Asp Asn Gln Glu Glu Glu Thr Ala Glu Asp				
	290		295	300
Leu Phe Glu Ile Asp Tyr Phe Gly Glu Lys Ile Glu Ile Ser Ile Asn				

305		310		315		320									
Val	Tyr	Tyr	Leu	Leu	Asp	Val	Ile	Asn	Asn	Ile	Lys	Ser	Glu	Asn	Ile
			325						330				335		
Ala	Leu	Phe	Leu	Asn	Lys	Ser	Lys	Ser	Ser	Ile	Gln	Ile	Glu	Ala	Glu
			340					345					350		
Asn	Asn	Ser	Ser	Asn	Ala	Tyr	Val	Val	Met	Leu	Leu	Lys	Arg		
		355						360				365			

<210> 114
 <211> 39
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 114
 gtgtggatcc tcgtccccct catgcgcgac caggaaggg 39

<210> 115
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 115
 gtgtggatcc gtggtgacct tagccac 27

<210> 116
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 116
 ttcgtgtccg aggaccttgt ggtccacaac 30

<210> 117
 <211> 3514
 <212> DNA
 <213> Aquifex aeolicus

<400> 117
 atgagtaagg atttcgtcca ccttcacctg cacacccagt tctcactcct ggacggggct 60
 ataaagatag acgagctcgt gaaaaaggca aaggagtatg gatacaaagc tgtcggaatg 120
 tcagaccacg gaaacctctt cggttcgtat aaattctaca aagccctgaa ggcggaagga 180
 attaagccca taatcgcat ggaagcctac ttaccacgg gttcgagggt tgacagaaag 240
 actaaaacga gcgaggacaa cataaccgac aagtacaacc accacctcat acttatagca 300
 aaggacgaaa aggtctaaag aacttaatga agctctcaac cctcgcctac aaagaagggt 360
 ttactacaa acccagaatt gattacgaac tccttgaaaa gtacggggag ggcctaatag 420
 cccttaccgc atgcctgaaa ggtgttccca cctactacgc ttctataaac gaagtgaaaa 480
 aggcggagga atgggtaaag aagttcaagg atatatcgg agatgacctt tatttagaac 540
 ttcaagcgaa caacattcca gaacaggaag tggcaaacag gaacttaata gagatagcca 600
 aaaagtacga tgtgaaactc atagcgacgc aggacgcccc ctacctcaat cccgaagaca 660
 ggtacgcccc cacggttctt atggcacttc aaatgaaaaa gaccattcac gaactgagtt 720
 cgggaaactt caagtgttca aacgaagacc ttactttgc tccacccgag tacatgtgga 780
 aaaagtttga aggttaagttc gaaggctggg aaaaggcact cctgaacact ctcgaggtaa 840
 tggaaaagac agcggacagc tttgagatat ttgaaaactc cacctacctc ctccccagt 900
 acgacgttcc gcccgacaaa acccttgagg aatacctcag agaactcgcg taaaagggtt 960
 taagacagag gatagaaagg ggacaagcta aggatactaa agagtactgg gagaggctcg 1020
 agtacgaact ggaagttata aacaaaatgg gctttgcggg atacttcttg atagttcagg 1080
 acttcataaa ctgggctaag aaaaacgaca tacctgttgg acccggaagg ggaagtgtcg 1140
 gaggttccct cgtcgcatac gccatcggaa taacggacgt tgaccctata aagcacggat 1200
 tcctttttga gaggttctta aaccccgaaa gggtttccat gccggatata gacgtggatt 1260
 tctgtcagga caacagggaa aaggctcatag agtacgtaag gaacaagtac ggacacgaca 1320
 acgtagctca gataatcacc tacaacgtaa tgaaggcgaa gcaaactg agagacgtcg 1380
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 gggacgttca gggaaacgtg ctcagtctgg aagagatgta caaaacgcct gtggaggaac 1500
 tccttcagaa gtacggagaa cacagaacgg acatagagga caacgtaaag aagttcagac 1560
 agatatcgga agaaagtccg gagataaaac agctcgttga gacggccctg aagcttgaag 1620
 gtctcacgag acacacctcc ctccacgccc cgggagtggg tatagcacca aagcccttga 1680
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 aactgaaact catgaaagaa ctcataaagg aaagacacgg agtgatata aacttcttg 1860
 aacttcccct tgacgacctg aaagtttaca aactccttca ggaaggaaaa accacgggag 1920
 tgttcagct cgaaagcagg ggaatgaaag aactcctgaa gaaactaaag cccgacagct 1980
 ttgacgacat cgttgcggtc ctgcactct acagaccgg acctctaaag agcggactcg 2040
 ttgacacata cattaagaga aagcacggaa aagaaccgt tgagtacccc ttcccgagc 2100
 ttgaaccgt ccttaaggaa acctacggag taatcgttta tcaggaacag gtgatgaaga 2160
 tgtctcagat actttccggc ttactcccg gagaggcgga taccctcaga aaggcgatag 2220
 gtaagaagaa agcggattta atggctcaga tgaaagacaa gttcatacag ggagcggtag 2280
 aaaggggata ccctgaagaa aagataagga agctctggga agacatagag aagttcgctt 2340
 ctactcctt caacaagtct cactcggtag cttacgggta catctcctac tggaccgct 2400
 acgttaaagc ccactatccc gcggagtct tgcggtaaa actcacaact gaaaagaacg 2460
 acaacaagtt cctcaacctc ataaaagacg ctaaactctt cggatttgag atacttcccc 2520

```

ccgacataaa caagagtgat gtaggattta c gatagaagg tgaaaacagg ataaggttcg 2580
ggcttgcgag gataaaggga gtgggagagg aaactgctaa gataatcggt gaagctagaa 2640
agaagtataa gcagttcaaa gggcttgcgg acttcataaa caaaaccaag aacaggaaga 2700
taaacaagaa agtcgtggaa gcaactcgtaa aggcaggggc ttttgacttt actaagaaaa 2760
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actccctttt cgggtgcaccg aaagaagaag tggaagaact cgaccctta aagcttgaaa 2880
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agaaccgcta cacaccatt gaagatttag aagagtggga caaggaaagc gaagcgggtgc 3000
ttacaggagt tatcacgga ctcaaagtaa aaaagacgaa aaacggagat tacatggcgg 3060
tcttcaacct cggtgacaag acgggactaa tagagtgtgt cgtcttcccg ggagtttacg 3120
aagaggcaaa ggaactgata gaagaggaca gagtagtggt agtcaaagg tttctggacg 3180
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tggttctcac gggtgatctg ggagactact tcgttgattt agcactcca caagatatga 3420
aactaaaggc tgacagaaag gttgtagagg agatagaaaa actgggagtg aaggtcataa 3480
ttagtaaat aacccttact tccgagtagt cccc 3514

```

<210> 118

<211> 1161

<212> PRT

<213> Aquifex aeolicus

<400> 118

```

Met Ser Lys Asp Phe Val His Leu His Leu His Thr Gln Phe Ser Leu
  1                      5                      10                      15

```

```

Leu Asp Gly Ala Ile Lys Ile Asp Glu Leu Val Lys Lys Ala Lys Glu
          20                      25                      30

```

```

Tyr Gly Tyr Lys Ala Val Gly Met Ser Asp His Gly Asn Leu Phe Gly
    35                      40                      45

```

```

Ser Tyr Lys Phe Tyr Lys Ala Leu Lys Ala Glu Gly Ile Lys Pro Ile
    50                      55                      60

```

```

Ile Gly Met Glu Ala Tyr Phe Thr Thr Gly Ser Arg Phe Asp Arg Lys
    65                      70                      75                      80

```

```

Thr Lys Thr Ser Glu Asp Asn Ile Thr Asp Lys Tyr Asn His His Leu
          85                      90                      95

```

```

Ile Leu Ile Ala Lys Asp Asp Lys Gly Leu Lys Asn Leu Met Lys Leu
    100                      105                      110

```

```

Ser Thr Leu Ala Tyr Lys Glu Gly Phe Tyr Tyr Lys Pro Arg Ile Asp
    115                      120                      125

```

Tyr Glu Leu Leu Glu Lys Tyr Gly Glu Gly Leu Ile Ala Leu Thr Ala
 130 135 140

Cys Leu Lys Gly Val Pro Thr Tyr Tyr Ala Ser Ile Asn Glu Val Lys
 145 150 155 160

Lys Ala Glu Glu Trp Val Lys Lys Phe Lys Asp Ile Phe Gly Asp Asp
 165 170 175

Leu Tyr Leu Glu Leu Gln Ala Asn Asn Ile Pro Glu Gln Glu Val Ala
 180 185 190

Asn Arg Asn Leu Ile Glu Ile Ala Lys Lys Tyr Asp Val Lys Leu Ile
 195 200 205

Ala Thr Gln Asp Ala His Tyr Leu Asn Pro Glu Asp Arg Tyr Ala His
 210 215 220

Thr Val Leu Met Ala Leu Gln Met Lys Lys Thr Ile His Glu Leu Ser
 225 230 235 240

Ser Gly Asn Phe Lys Cys Ser Asn Glu Asp Leu His Phe Ala Pro Pro
 245 250 255

Glu Tyr Met Trp Lys Lys Phe Glu Gly Lys Phe Glu Gly Trp Glu Lys
 260 265 270

Ala Leu Leu Asn Thr Leu Glu Val Met Glu Lys Thr Ala Asp Ser Phe
 275 280 285

Glu Ile Phe Glu Asn Ser Thr Tyr Leu Leu Pro Lys Tyr Asp Val Pro
 290 295 300

Pro Asp Lys Thr Leu Glu Glu Tyr Leu Arg Glu Leu Ala Tyr Lys Gly
 305 310 315 320

Leu Arg Gln Arg Ile Glu Arg Gly Gln Ala Lys Asp Thr Lys Glu Tyr
 325 330 335

Trp Glu Arg Leu Glu Tyr Glu Leu Glu Val Ile Asn Lys Met Gly Phe
 340 345 350

Ala Gly Tyr Phe Leu Ile Val Gln Asp Phe Ile Asn Trp Ala Lys Lys
 355 360 365

Asn Asp Ile Pro Val Gly Pro Gly Arg Gly Ser Ala Gly Gly Ser Leu
 370 375 380

Val	Ala	Tyr	Ala	Ile	Gly	Ile	Thr	Asp	Val	Asp	Pro	Ile	Lys	His	Gly	385	390	395	400
Phe	Leu	Phe	Glu	Arg	Phe	Leu	Asn	Pro	Glu	Arg	Val	Ser	Met	Pro	Asp	405	410	415	
Ile	Asp	Val	Asp	Phe	Cys	Gln	Asp	Asn	Arg	Glu	Lys	Val	Ile	Glu	Tyr	420	425	430	
Val	Arg	Asn	Lys	Tyr	Gly	His	Asp	Asn	Val	Ala	Gln	Ile	Ile	Thr	Tyr	435	440	445	
Asn	Val	Met	Lys	Ala	Lys	Gln	Thr	Leu	Arg	Asp	Val	Ala	Arg	Ala	Met	450	455	460	
Gly	Leu	Pro	Tyr	Ser	Thr	Ala	Asp	Lys	Leu	Ala	Lys	Leu	Ile	Pro	Gln	465	470	475	480
Gly	Asp	Val	Gln	Gly	Thr	Trp	Leu	Ser	Leu	Glu	Glu	Met	Tyr	Lys	Thr	485	490	495	
Pro	Val	Glu	Glu	Leu	Leu	Gln	Lys	Tyr	Gly	Glu	His	Arg	Thr	Asp	Ile	500	505	510	
Glu	Asp	Asn	Val	Lys	Lys	Phe	Arg	Gln	Ile	Cys	Glu	Glu	Ser	Pro	Glu	515	520	525	
Ile	Lys	Gln	Leu	Val	Glu	Thr	Ala	Leu	Lys	Leu	Glu	Gly	Leu	Thr	Arg	530	535	540	
His	Thr	Ser	Leu	His	Ala	Ala	Gly	Val	Val	Ile	Ala	Pro	Lys	Pro	Leu	545	550	555	560
Ser	Glu	Leu	Val	Pro	Leu	Tyr	Tyr	Asp	Lys	Glu	Gly	Glu	Val	Ala	Thr	565	570	575	
Gln	Tyr	Asp	Met	Val	Gln	Leu	Glu	Glu	Leu	Gly	Leu	Leu	Lys	Met	Asp	580	585	590	
Phe	Leu	Gly	Leu	Lys	Thr	Leu	Thr	Glu	Leu	Lys	Leu	Met	Lys	Glu	Leu	595	600	605	
Ile	Lys	Glu	Arg	His	Gly	Val	Asp	Ile	Asn	Phe	Leu	Glu	Leu	Pro	Leu	610	615	620	
Asp	Asp	Pro	Lys	Val	Tyr	Lys	Leu	Leu	Gln	Glu	Gly	Lys	Thr	Thr	Gly	625	630	635	640

Val	Phe	Gln	Leu	Glu	Ser	Arg	Gly	Met	Lys	Glu	Leu	Leu	Lys	Lys	Leu	645	650	655
Lys	Pro	Asp	Ser	Phe	Asp	Asp	Ile	Val	Ala	Val	Leu	Ala	Leu	Tyr	Arg	660	665	670
Pro	Gly	Pro	Leu	Lys	Ser	Gly	Leu	Val	Asp	Thr	Tyr	Ile	Lys	Arg	Lys	675	680	685
His	Gly	Lys	Glu	Pro	Val	Glu	Tyr	Pro	Phe	Pro	Glu	Leu	Glu	Pro	Val	690	695	700
Leu	Lys	Glu	Thr	Tyr	Gly	Val	Ile	Val	Tyr	Gln	Glu	Gln	Val	Met	Lys	705	710	715
Met	Ser	Gln	Ile	Leu	Ser	Gly	Phe	Thr	Pro	Gly	Glu	Ala	Asp	Thr	Leu	725	730	735
Arg	Lys	Ala	Ile	Gly	Lys	Lys	Lys	Ala	Asp	Leu	Met	Ala	Gln	Met	Lys	740	745	750
Asp	Lys	Phe	Ile	Gln	Gly	Ala	Val	Glu	Arg	Gly	Tyr	Pro	Glu	Glu	Lys	755	760	765
Ile	Arg	Lys	Leu	Trp	Glu	Asp	Ile	Glu	Lys	Phe	Ala	Ser	Tyr	Ser	Phe	770	775	780
Asn	Lys	Ser	His	Ser	Val	Ala	Tyr	Gly	Tyr	Ile	Ser	Tyr	Trp	Thr	Ala	785	790	795
Tyr	Val	Lys	Ala	His	Tyr	Pro	Ala	Glu	Phe	Phe	Ala	Val	Lys	Leu	Thr	805	810	815
Thr	Glu	Lys	Asn	Asp	Asn	Lys	Phe	Leu	Asn	Leu	Ile	Lys	Asp	Ala	Lys	820	825	830
Leu	Phe	Gly	Phe	Glu	Ile	Leu	Pro	Pro	Asp	Ile	Asn	Lys	Ser	Asp	Val	835	840	845
Gly	Phe	Thr	Ile	Glu	Gly	Glu	Asn	Arg	Ile	Arg	Phe	Gly	Leu	Ala	Arg	850	855	860
Ile	Lys	Gly	Val	Gly	Glu	Glu	Thr	Ala	Lys	Ile	Ile	Val	Glu	Ala	Arg	865	870	875
Lys	Lys	Tyr	Lys	Gln	Phe	Lys	Gly	Leu	Ala	Asp	Phe	Ile	Asn	Lys	Thr	885	890	895

Lys Asn Arg Lys Ile Asn Lys Lys Val Val Glu Ala Leu Val Lys Ala
 900 905 910
 Gly Ala Phe Asp Phe Thr Lys Lys Lys Arg Lys Glu Leu Leu Ala Lys
 915 920 925
 Val Ala Asn Ser Glu Lys Ala Leu Met Ala Thr Gln Asn Ser Leu Phe
 930 935 940
 Gly Ala Pro Lys Glu Glu Val Glu Glu Leu Asp Pro Leu Lys Leu Glu
 945 950 955 960
 Lys Glu Val Leu Gly Phe Tyr Ile Ser Gly His Pro Leu Asp Asn Tyr
 965 970 975
 Glu Lys Leu Leu Lys Asn Arg Tyr Thr Pro Ile Glu Asp Leu Glu Glu
 980 985 990
 Trp Asp Lys Glu Ser Glu Ala Val Leu Thr Gly Val Ile Thr Glu Leu
 995 1000 1005
 Lys Val Lys Lys Thr Lys Asn Gly Asp Tyr Met Ala Val Phe Asn Leu
 1010 1015 1020
 Val Asp Lys Thr Gly Leu Ile Glu Cys Val Val Phe Pro Gly Val Tyr
 1025 1030 1035 1040
 Glu Glu Ala Lys Glu Leu Ile Glu Glu Asp Arg Val Val Val Val Lys
 1045 1050 1055
 Gly Phe Leu Asp Glu Asp Leu Glu Thr Glu Asn Val Lys Phe Val Val
 1060 1065 1070
 Lys Glu Val Phe Ser Pro Glu Glu Phe Ala Lys Glu Met Arg Asn Thr
 1075 1080 1085
 Leu Tyr Ile Phe Leu Lys Arg Glu Gln Ala Leu Asn Gly Val Ala Glu
 1090 1095 1100
 Lys Leu Lys Gly Ile Ile Glu Asn Asn Arg Thr Glu Asp Gly Tyr Asn
 1105 1110 1115 1120
 Leu Val Leu Thr Val Asp Leu Gly Asp Tyr Phe Val Asp Leu Ala Leu
 1125 1130 1135
 Pro Gln Asp Met Lys Leu Lys Ala Asp Arg Lys Val Val Glu Glu Ile
 1140 1145 1150

Glu Lys Leu Gly Val Lys Val Ile Ile
 1155 1160

<210> 119
 <211> 2408
 <212> DNA
 <213> Aquifex aeolicus

<400> 119
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 tacctctttg ccggaccgag gggggttggg aagacgacta ttgcaagaat tctcgcaaaa 180
 gctttgaact gtaaaaatcc ctccaaagggt gagccctgcg gtgagtgcga aaactgcagg 240
 gagatagaca ggggtgtgtt ccctgactta attgaaatgg atgccgcctc aaacaggggt 300
 atagacgacg taagggcatt aaaagaagcg gtcaattaca aacctataaa aggaaagtac 360
 aaggtttaca taatagacga agctcacatg ctcacgaaag aagctttcaa cgctctctta 420
 aaaaccctcg aagagccccc tcccagaact gttttcgtcc tttgtaccac ggagtacgac 480
 aaaattcttc ccacgatact ctcaagggtg cagaggataa tcttctcaaa ggtaagaaag 540
 gaaaaagtaa tagagtatct aaaaaagata tgtgaaaagg aagggttga gtgcgaagag 600
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 gtggacgaag ctataaagtt cctcagagaa ctctcagaaa agggctacaa cctgaccaag 840
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 gccctcctct acgttgagaa cctgataaac aggggtaaaag ttgaagcgag aacgagagaa 1020
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agaggggctac cttctcgggtt aggggagacg tgggttgagat agtcccttct cacacggaag 2340
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ctctgaac 2408

<210> 120

<211> 473

<212> PRT

<213> Aquifex aeolicus

<400> 120

Met Asn Tyr Val Pro Phe Ala Arg Lys Tyr Arg Pro Lys Phe Phe Arg
1 5 10 15

Glu Val Ile Gly Gln Glu Ala Pro Val Arg Ile Leu Lys Asn Ala Ile
20 25 30

Lys Asn Asp Arg Val Ala His Ala Tyr Leu Phe Ala Gly Pro Arg Gly
35 40 45

Val Gly Lys Thr Thr Ile Ala Arg Ile Leu Ala Lys Ala Leu Asn Cys
50 55 60

Lys Asn Pro Ser Lys Gly Glu Pro Cys Gly Glu Cys Glu Asn Cys Arg
65 70 75 80

Glu Ile Asp Arg Gly Val Phe Pro Asp Leu Ile Glu Met Asp Ala Ala
85 90 95

Ser Asn Arg Gly Ile Asp Asp Val Arg Ala Leu Lys Glu Ala Val Asn
100 105 110

Tyr Lys Pro Ile Lys Gly Lys Tyr Lys Val Tyr Ile Ile Asp Glu Ala
115 120 125

His Met Leu Thr Lys Glu Ala Phe Asn Ala Leu Leu Lys Thr Leu Glu
130 135 140

Glu Pro Pro Pro Arg Thr Val Phe Val Leu Cys Thr Thr Glu Tyr Asp
145 150 155 160

Lys Ile Leu Pro Thr Ile Leu Ser Arg Cys Gln Arg Ile Ile Phe Ser
165 170 175

Lys Val Arg Lys Glu Lys Val Ile Glu Tyr Leu Lys Lys Ile Cys Glu
180 185 190

Lys Glu Gly Ile Glu Cys Glu Glu Gly Ala Leu Glu Val Leu Ala His
 195 200 205
 Ala Ser Glu Gly Cys Met Arg Asp Ala Ala Ser Leu Leu Asp Gln Ala
 210 215 220
 Ser Val Tyr Gly Glu Gly Arg Val Thr Lys Glu Val Val Glu Asn Phe
 225 230 235 240
 Leu Gly Ile Leu Ser Gln Glu Ser Val Arg Ser Phe Leu Lys Leu Leu
 245 250 255
 Leu Asn Ser Glu Val Asp Glu Ala Ile Lys Phe Leu Arg Glu Leu Ser
 260 265 270
 Glu Lys Gly Tyr Asn Leu Thr Lys Phe Trp Glu Met Leu Glu Glu Glu
 275 280 285
 Val Arg Asn Ala Ile Leu Val Lys Ser Leu Lys Asn Pro Glu Ser Val
 290 295 300
 Val Gln Asn Trp Gln Asp Tyr Glu Asp Phe Lys Asp Tyr Pro Leu Glu
 305 310 315 320
 Ala Leu Leu Tyr Val Glu Asn Leu Ile Asn Arg Gly Lys Val Glu Ala
 325 330 335
 Arg Thr Arg Glu Pro Leu Arg Ala Phe Glu Leu Ala Val Ile Lys Ser
 340 345 350
 Leu Ile Val Lys Asp Ile Ile Pro Val Ser Gln Leu Gly Ser Val Val
 355 360 365
 Lys Glu Thr Lys Lys Glu Glu Lys Lys Val Glu Val Lys Glu Glu Pro
 370 375 380
 Lys Val Lys Glu Glu Lys Pro Lys Glu Gln Glu Glu Asp Arg Phe Gln
 385 390 395 400
 Lys Val Leu Asn Ala Val Asp Gly Lys Ile Leu Lys Arg Ile Leu Glu
 405 410 415
 Gly Ala Lys Arg Glu Glu Arg Asp Gly Lys Ile Val Leu Lys Ile Glu
 420 425 430
 Ala Ser Tyr Leu Arg Thr Met Lys Lys Glu Phe Asp Ser Leu Lys Glu
 435 440 445

Thr Phe Pro Phe Leu Glu Phe Glu Pro Val Glu Asp Lys Lys Lys Pro
 450 455 460

Gln Lys Ser Ser Gly Thr Arg Leu Phe
 465 470

<210> 121
 <211> 1090
 <212> DNA
 <213> Aquifex aeolicus

<400> 121
 atgcgcggtta aggtggacag ggaggagctt gaagagggtt ttaaaaaagc aagagaaagc 60
 acggaaaaaaa aagccgcact cccgatactc gcgaacttct tactctccgc aaaagaggaa 120
 aacttaatcg taagggcaac ggacttggaa aactaccttg tagtctccgt aaagggggag 180
 gttgaagagg aaggagaggt ttgcgtccac tctcaaaaac tctacgatat agtcaagaac 240
 ttaaattccg cttacgttta ctttcatacg gaagggtgaaa aactcgtcat aacgggagga 300
 aagagtacgt acaaacttcc gacagctccc gcggaggact ttcccgaatt tccagaaatc 360
 gtagaaggag gagaaacact ttcgggaaac cttctcgtta acggaataga aaaggtagag 420
 tacgccatag cgaaggaaga agcgaacata gcccttcagg gaatgtatct gagaggatac 480
 gaggacagaa ttcactttgt gttcggacgg tcacaggctt gcactttatg aacctctacg 540
 taaacattga aaagagtga gacgagtctt ttgcttactt ctccactccc gagtggaaac 600
 tcgccggttag ctccctggaag gagaattccc ggactacatg agtgtcatcc ctgaggagtt 660
 ttcggcgga gtcctgtttg agacagagga agtcttaaag gttttaaaga ggttgaaggc 720
 tttaagcgaa ggaaaagttt ttcccggtgaa gattacctta agcgaaaacc ttgccatctt 780
 tgagttcgcg gatccggagt tcggagaagc gagagaggaa attgaagtgg agtacacggg 840
 agagcccttt gagataggat tcaacggaaa taccttatgg aggcgcttga cgcctacgac 900
 agcgaaagag tgtggttcaa gttcacaacc cccgacacgg ccactttatt ggaggctgaa 960
 gattacgaaa aggaacctta caagtgcata ataatgccga tgagggtgta gccatgaaaa 1020
 aagctttaat ctttttattg agcttgagcc ttttaattcc tgcgttttagc gaagccaaac 1080
 ccaagtcttc 1090

<210> 122
 <211> 363
 <212> PRT
 <213> Aquifex aeolicus

<400> 122
 Met Arg Val Lys Val Asp Arg Glu Glu Leu Glu Glu Val Leu Lys Lys
 1 5 10 15

Ala Arg Glu Ser Thr Glu Lys Lys Ala Ala Leu Pro Ile Leu Ala Asn
 20 25 30

Phe Leu Leu Ser Ala Lys Glu Glu Asn Leu Ile Val Arg Ala Thr Asp
 35 40 45

Leu Glu Asn Tyr Leu Val Val Ser Val Lys Gly Glu Val Glu Glu Glu
 50 55 60

Gly Glu Val Cys Val His Ser Gln Lys Leu Tyr Asp Ile Val Lys Asn
 65 70 75 80

Leu Asn Ser Ala Tyr Val Tyr Leu His Thr Glu Gly Glu Lys Leu Val
 85 90 95

Ile Thr Gly Gly Lys Ser Thr Tyr Lys Leu Pro Thr Ala Pro Ala Glu
 100 105 110

Asp Phe Pro Glu Phe Pro Glu Ile Val Glu Gly Gly Glu Thr Leu Ser
 115 120 125

Gly Asn Leu Leu Val Asn Gly Ile Glu Lys Val Glu Tyr Ala Ile Ala
 130 135 140

Lys Glu Glu Ala Asn Ile Ala Leu Gln Gly Met Tyr Leu Arg Gly Tyr
 145 150 155 160

Glu Asp Arg Ile His Phe Val Gly Ser Asp Gly His Arg Leu Ala Leu
 165 170 175

Tyr Glu Pro Leu Gly Glu Phe Ser Lys Glu Leu Leu Ile Pro Arg Lys
 180 185 190

Ser Leu Lys Val Leu Lys Lys Leu Ile Thr Gly Ile Glu Asp Val Asn
 195 200 205

Ile Glu Lys Ser Glu Asp Glu Ser Phe Ala Tyr Phe Ser Thr Pro Glu
 210 215 220

Trp Lys Leu Ala Val Arg Leu Leu Glu Gly Glu Phe Pro Asp Tyr Met
 225 230 235 240

Ser Val Ile Pro Glu Glu Phe Ser Ala Glu Val Leu Phe Glu Thr Glu
 245 250 255

Glu Val Leu Lys Val Leu Lys Arg Leu Lys Ala Leu Ser Glu Gly Lys
 260 265 270

Val Phe Pro Val Lys Ile Thr Leu Ser Glu Asn Leu Ala Ile Phe Glu
 275 280 285

Phe Ala Asp Pro Glu Phe Gly Glu Ala Arg Glu Glu Ile Glu Val Glu
 290 295 300

Tyr Thr Gly Glu Pro Phe Glu Ile Gly Phe Asn Gly Lys Tyr Leu Met
 305 310 315 320

Glu Ala Leu Asp Ala Tyr Asp Ser Glu Arg Val Trp Phe Lys Phe Thr
 325 330 335

Thr Pro Asp Thr Ala Thr Leu Leu Glu Ala Glu Asp Tyr Glu Lys Glu
 340 345 350

Pro Tyr Lys Cys Ile Ile Met Pro Met Arg Val
 355 360

<210> 123
 <211> 1093
 <212> DNA
 <213> Aquifex aeolicus

<400> 123
 gtggaaccca caatattcca gttccagaaa acttttttca caaacctcc gaaggagagg 60
 gtcttcgtcc ttcattggaga agagcagtat ctcataagaa cctttttgtc taagctgaag 120
 gaaaagtacg gggagaatta cacggttctg tgggggggatg agataagcga ggaggaattc 180
 tacactgccc tttccgagac cagtatatcc ggcggttcaa aggaaaaagc ggtggtcatt 240
 tacaacttcg gggatttcct gaagaagctc ggaaggaaga aaaaggaaaa agaaaggctt 300
 ataaaagtcc tcagaaacgt aaagagtaac tacgtattta tagtgtacga tgcgaaactc 360
 cagaaacagg aacttttctc ggaacctctg aaatccgtag cgtctttcgg cggatatagt 420
 gtagcaaaca ggctgagcaa ggagaggata aaacagctcg tccttaagaa gttcaaagaa 480
 aaagggataa acgtagaaaa cgatgcctt gaatacctc tccagctcac ggggttacaac 540
 ttgatggagc tcaaacttga ggttgaaaaa ctgatagatt acgcaagtga aaagaaaatt 600
 ttaacactcg atgaggtaaa gagagtagcc ttctcagtct cagaaaacgt aaacgtattt 660
 gagttcgttg atttactcct cttaaaagat tacgaaaagg ctcttaaagt tttggactcc 720
 ctcatctcct tcggaatata cccctccag attatgaaaa tcctgtcctc ctatgctcta 780
 aaactttaca ccctcaagag gcttgaagag aaggagagg acctgaataa ggcgatggaa 840
 agcgtgggaa taaagaacaa ctttctcaag atgaagttca aatcttactt aaaggcaaac 900
 tctaaagagg acttgaagaa cctaactctc tccctccaga ggatagacgc tttttctaaa 960
 ctttactttc aggacacagt gcagttgctg gggatttctt gacctcaaga ctggagaggg 1020
 aagttgtgaa aaatacttct catggtggat aatctttttt atgaagtttg cggtttgcgt 1080
 ttttcccggt tct 1093

<210> 124
 <211> 350
 <212> PRT
 <213> Aquifex aeolicus

<400> 124
 Val Glu Thr Thr Ile Phe Gln Phe Gln Lys Thr Phe Phe Thr Lys Pro

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Pro Lys Glu Arg Val Phe Val Leu His Gly Glu Glu Gln Tyr Leu Ile			
20	25	30	
Arg Thr Phe Leu Ser Lys Leu Lys Glu Lys Tyr Gly Glu Asn Tyr Thr			
35	40	45	
Val Leu Trp Gly Asp Glu Ile Ser Glu Glu Glu Phe Tyr Thr Ala Leu			
50	55	60	
Ser Glu Thr Ser Ile Phe Gly Gly Ser Lys Glu Lys Ala Val Val Ile			
65	70	75	80
Tyr Asn Phe Gly Asp Phe Leu Lys Lys Leu Gly Arg Lys Lys Lys Glu			
85	90	95	
Lys Glu Arg Leu Ile Lys Val Leu Arg Asn Val Lys Ser Asn Tyr Val			
100	105	110	
Phe Ile Val Tyr Asp Ala Lys Leu Gln Lys Gln Glu Leu Ser Ser Glu			
115	120	125	
Pro Leu Lys Ser Val Ala Ser Phe Gly Gly Ile Val Val Ala Asn Arg			
130	135	140	
Leu Ser Lys Glu Arg Ile Lys Gln Leu Val Leu Lys Lys Phe Lys Glu			
145	150	155	160
Lys Gly Ile Asn Val Glu Asn Asp Ala Leu Glu Tyr Leu Leu Gln Leu			
165	170	175	
Thr Gly Tyr Asn Leu Met Glu Leu Lys Leu Glu Val Glu Lys Leu Ile			
180	185	190	
Asp Tyr Ala Ser Glu Lys Lys Ile Leu Thr Leu Asp Glu Val Lys Arg			
195	200	205	
Val Ala Phe Ser Val Ser Glu Asn Val Asn Val Phe Glu Phe Val Asp			
210	215	220	
Leu Leu Leu Leu Lys Asp Tyr Glu Lys Ala Leu Lys Val Leu Asp Ser			
225	230	235	240
Leu Ile Ser Phe Gly Ile His Pro Leu Gln Ile Met Lys Ile Leu Ser			
245	250	255	
Ser Tyr Ala Leu Lys Leu Tyr Thr Leu Lys Arg Leu Glu Glu Lys Gly			

260	265	270
Glu Asp Leu Asn Lys Ala Met Glu Ser Val Gly Ile Lys Asn Asn Phe		
275	280	285
Leu Lys Met Lys Phe Lys Ser Tyr Leu Lys Ala Asn Ser Lys Glu Asp		
290	295	300
Leu Lys Asn Leu Ile Leu Ser Leu Gln Arg Ile Asp Ala Phe Ser Lys		
305	310	315
320		
Leu Tyr Phe Gln Asp Thr Val Gln Leu Leu Arg Asp Phe Leu Thr Ser		
325	330	335
Arg Leu Glu Arg Glu Val Val Lys Asn Thr Ser His Gly Gly		
340	345	350

<210> 125
 <211> 1051
 <212> DNA
 <213> Aquifex aeolicus

<400> 125

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atggaaaaag tttttttgga aaaactccag aaaaccttgc acatacccgg aggactcctt 60
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ttatgtaagg aaaacgtacc tggggatgcg gaagttgtcc ctcttgcaaa cacgtaaacy 180
agctggagga agccttcttt aaaggagaaa tagaagactt taaagtttat aagacaagga 240
cggtaaaaag cacttcgttt accttatggg cgaacatccc gactttgtgg taataatccc 300
gagcggacat tacataaaga tagaacagat aagggaagtt aagaactttg cctatgtgaa 360
gcccgcacta agcaggagaa aagtaattat aatagacgac gccacgcga tgacctctca 420
ggcggcaaac gctcttttaa aggtattgga agagccacct gcggacacca cctttatctt 480
gaccacgaac aggcgttctg caatcctgcc gactatcctc tccagaactt ttcaagtgga 540
gttcaagggc ttttcagtaa aagaggttat ggaaatagcg aaagtagacg aggaaatagc 600
gaaactctct ggaggcagtc taaaaagggc tatcttacta aaggaaaaca aagatatcct 660
aaacaaagta aaggaattct tggaaaacga gccgttaaaa gtttacaagc ttgcaagtga 720
attcgaaaag tgggaacctg aaaagcaaaa actcttcctt gaaattatgg aagaattggt 780
atctcaaaaa ttgaccgaag agaaaaaaga caattacacc taccttcttg atacgatcag 840
actctttaa gacggactcg caaggggtgt aaacgaacct ctgtggctgt ttacgttagc 900
cgttcaggcg gattaataaa ccgttattga ttccgtaaca tttaaacctt aatctaaatt 960
atgagagcct ttgaaggagg tctggtatgg aaaatttgaa gattagatat atagatacga 1020
ggaagatagg aaccgtgagc ggtgtaaaag t                                     1051

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<210> 126
 <211> 305
 <212> PRT
 <213> Aquifex aeolicus

<400> 126

Met Glu Lys Val Phe Leu Glu Lys Leu Gln Lys Thr Leu His Ile Pro
1 5 10 15

Gly Gly Leu Leu Phe Tyr Gly Lys Glu Gly Ser Gly Lys Thr Lys Thr
20 25 30

Ala Phe Glu Phe Ala Lys Gly Ile Leu Cys Lys Glu Asn Val Pro Trp
35 40 45

Gly Cys Gly Ser Cys Pro Ser Cys Lys His Val Asn Glu Leu Glu Glu
50 55 60

Ala Phe Phe Lys Gly Glu Ile Glu Asp Phe Lys Val Tyr Lys Asp Lys
65 70 75 80

Asp Gly Lys Lys His Phe Val Tyr Leu Met Gly Glu His Pro Asp Phe
85 90 95

Val Val Ile Ile Pro Ser Gly His Tyr Ile Lys Ile Glu Gln Ile Arg
100 105 110

Glu Val Lys Asn Phe Ala Tyr Val Lys Pro Ala Leu Ser Arg Arg Lys
115 120 125

Val Ile Ile Ile Asp Asp Ala His Ala Met Thr Ser Gln Ala Ala Asn
130 135 140

Ala Leu Leu Lys Val Leu Glu Glu Pro Pro Ala Asp Thr Thr Phe Ile
145 150 155 160

Leu Thr Thr Asn Arg Arg Ser Ala Ile Leu Pro Thr Ile Leu Ser Arg
165 170 175

Thr Phe Gln Val Glu Phe Lys Gly Phe Ser Val Lys Glu Val Met Glu
180 185 190

Ile Ala Lys Val Asp Glu Glu Ile Ala Lys Leu Ser Gly Gly Ser Leu
195 200 205

Lys Arg Ala Ile Leu Leu Lys Glu Asn Lys Asp Ile Leu Asn Lys Val
210 215 220

Lys Glu Phe Leu Glu Asn Glu Pro Leu Lys Val Tyr Lys Leu Ala Ser
225 230 235 240

Glu Phe Glu Lys Trp Glu Pro Glu Lys Gln Lys Leu Phe Leu Glu Ile

245 250 255
 Met Glu Glu Leu Val Ser Gln Lys Leu Thr Glu Glu Lys Lys Asp Asn
 260 265 270
 Tyr Thr Tyr Leu Leu Asp Thr Ile Arg Leu Phe Lys Asp Gly Leu Ala
 275 280 285
 Arg Gly Val Asn Glu Pro Leu Trp Leu Phe Thr Leu Ala Val Gln Ala
 290 295 300
 Asp
 305

<210> 127
 <211> 630
 <212> DNA
 <213> Aquifex aeolicus

<400> 127
 atgaacttcc tgaaaaagtt ccttttactg agaaaagctc aaaagtctcc ttacttcgaa 60
 gagttctacg aagaaatcga tttgaaccag aagggtgaaag atgcaagggt tgtagttttt 120
 gactgcgaag ccacagaact cgacgtaaaag aaggcaaaac tcctttcaat aggtgcggtt 180
 gaggttaaaa acctggaaat agacctctct aaatcttttt acgagatact caaaagtgcac 240
 gagataaagg cggcgggagat acatggaata accagggaag acgttgaaaa gtacggaaaag 300
 gaaccaaagg aagtaatata cgactttctg aagtacataa agggaagcgt tctcgttggc 360
 tactacgtga agtttgacgt ctactcgtt gagaagtact ccataaagta cttccagtat 420
 ccaatcatca actacaagtt agacctgttt agtttcgtga agagagagta ccagagtggc 480
 aggagtcttg acgaccttat gaaggaactc ggtgtagaaa taagggaag gcacaacgcc 540
 cttgaagatg cctacataac cgctcttctt ttcctaaagt acgtttaccc gaacagggag 600
 tacagactaa aggatctccc gattttcctt 630

<210> 128
 <211> 210
 <212> PRT
 <213> Aquifex aeolicus

<400> 128
 Met Asn Phe Leu Lys Lys Phe Leu Leu Leu Arg Lys Ala Gln Lys Ser
 1 5 10 15
 Pro Tyr Phe Glu Glu Phe Tyr Glu Glu Ile Asp Leu Asn Gln Lys Val
 20 25 30
 Lys Asp Ala Arg Phe Val Val Phe Asp Cys Glu Ala Thr Glu Leu Asp
 35 40 45

Val Lys Lys Ala Lys Leu Leu Ser Ile Gly Ala Val Glu Val Lys Asn
 50 55 60
 Leu Glu Ile Asp Leu Ser Lys Ser Phe Tyr Glu Ile Leu Lys Ser Asp
 65 70 75 80
 Glu Ile Lys Ala Ala Glu Ile His Gly Ile Thr Arg Glu Asp Val Glu
 85 90 95
 Lys Tyr Gly Lys Glu Pro Lys Glu Val Ile Tyr Asp Phe Leu Lys Tyr
 100 105 110
 Ile Lys Gly Ser Val Leu Val Gly Tyr Tyr Val Lys Phe Asp Val Ser
 115 120 125
 Leu Val Glu Lys Tyr Ser Ile Lys Tyr Phe Gln Tyr Pro Ile Ile Asn
 130 135 140
 Tyr Lys Leu Asp Leu Phe Ser Phe Val Lys Arg Glu Tyr Gln Ser Gly
 145 150 155 160
 Arg Ser Leu Asp Asp Leu Met Lys Glu Leu Gly Val Glu Ile Arg Ala
 165 170 175
 Arg His Asn Ala Leu Glu Asp Ala Tyr Ile Thr Ala Leu Leu Phe Leu
 180 185 190
 Lys Tyr Val Tyr Pro Asn Arg Glu Tyr Arg Leu Lys Asp Leu Pro Ile
 195 200 205
 Phe Leu
 210

<210> 129

<211> 526

<212> DNA

<213> Aquifex aeolicus

<400> 129

atgctcaata aggtttttat aataggaaga cttacgggtg accccgttat aacttatcta 60
 ccgagcgga cgcccgtagt agagtttact ctggcttaca acagaaggta taaaaaccag 120
 aacggtgaat ttcaggagga aagtcacttc tttgacgtaa aggcgtacgg aaaaatggct 180
 gaagactggg ctacacgctt ctcgaaagga tacctcgtac tcgtagaggg aagactctcc 240
 caggaaaagt gggagaaaga aggaaagaag ttctcaaagg tcaggataat agcggaaaac 300
 gtaagattaa taaacaggcc gaaagggtgct gaacttcaag cagaagaaga ggaggaagtt 360
 cctcccattg aggaggaaat tgaaaaactc ggtaaagagg aagagaagcc ttttaccgat 420

gaagaggacg aaataccttt ttaattttga ggagggttaa gtatggtagt gagagctcct 480
aagaagaaag tttgtatgta ctgtgaacaa aagagagagc cagatt 526

<210> 130

<211> 147

<212> PRT

<213> Aquifex aeolicus

<400> 130

Met Leu Asn Lys Val Phe Ile Ile Gly Arg Leu Thr Gly Asp Pro Val
1 5 10 15

Ile Thr Tyr Leu Pro Ser Gly Thr Pro Val Val Glu Phe Thr Leu Ala
20 25 30

Tyr Asn Arg Arg Tyr Lys Asn Gln Asn Gly Glu Phe Gln Glu Glu Ser
35 40 45

His Phe Phe Asp Val Lys Ala Tyr Gly Lys Met Ala Glu Asp Trp Ala
50 55 60

Thr Arg Phe Ser Lys Gly Tyr Leu Val Leu Val Glu Gly Arg Leu Ser
65 70 75 80

Gln Glu Lys Trp Glu Lys Glu Gly Lys Lys Phe Ser Lys Val Arg Ile
85 90 95

Ile Ala Glu Asn Val Arg Leu Ile Asn Arg Pro Lys Gly Ala Glu Leu
100 105 110

Gln Ala Glu Glu Glu Glu Glu Val Pro Pro Ile Glu Glu Glu Ile Glu
115 120 125

Lys Leu Gly Lys Glu Glu Glu Lys Pro Phe Thr Asp Glu Glu Asp Glu
130 135 140

Ile Pro Phe
145

<210> 131

<211> 1472

<212> DNA

<213> Aquifex aeolicus

<400> 131

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atgcttgaag accccgaaaa catacctctg gtacttgaat accttaaaga agaagacttc 120
tgcatagacg agcacaagct acttttcagg gttcttataa acctctgggc cgagtacggc 180
aataagctcg atttcgtatt aataaaggat caccttgaaa agaaaaactt actccagaaa 240
atacctatag actggctcga agaactctac gaggaggcgg tatcccctga cacgcttgag 300
gaagtctgca aaatagtaaa acaacgttcc gcacagaggg cgataattca actcgggtata 360
gaactcattc acaaaggaaa ggaaaacaaa gactttcaca cattaatcga ggaagccag 420
agcaggatat tttccatagc ggaaagtgtc acatctacgc agttttacca tgtgaaagac 480
gttgcggaag aagttataga actcatttat aaattcaaaa gctctgacag gctagtcacg 540
ggactcccaa gcggtttcac ggaactcgat cttaaagacga cgggattcca ccctggagac 600
ttaataatac tcgccgcaag acccggtatg gggaaaaccg cctttatgct ctccataatc 660
tacaatctcg caaaagacga gggaaaaccc tcagctgtat tttccttga aatgagcaag 720
gaacagctcg ttatgagact cctctctatg atgtcggagg tcccactttt caagataagg 780
tctggaagta tatcgaatga agatttaaag aagcttgaag caagcgcaat agaactcgca 840
aagtacgaca tatacctcga cgacacaccc gctctcacta caacggattt aaggataagg 900
gcaagaaaagc tcagaaagga aaaggaagtt gagttcgtgg cgggtggacta cttgcaactt 960
ctgagaccgc cagtccgaaa gagttcaaga caggaggaag tggcagaggt ttcaagaaac 1020
ttaaaagccc ttgcaaagga acttcacatt cccgttatgg cacttgcgca gctctccgt 1080
gaggtggaaa agaggagtga taaaagaccc cagcttgagg acctcagaga atccggacag 1140
atagaacagg acgcagacct aatccttttc ctccacagac ccgagtacta caagaaaaag 1200
ccaaatcccg aagagcaggg tatagcggaa gtgataatag ccaagcaaag gcaaggaccc 1260
acggacattg tgaagctcgc atttattaag gagtacacta agtttgcaa cctagaagcc 1320
cttcctgaac aacctcctga agaagaggaa ctttccgaaa ttattgaaac acaggaggat 1380
gaaggattcg aagatattga cttctgaaaa ttaaggtttt ataattttat cttggctatc 1440
cggggtagct caatcggcag agcgggtggc tg 1472

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<210> 132

<211> 438

<212> PRT

<213> Aquifex aeolicus

<400> 132

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Met Gln Phe Val Asp Lys Leu Pro Cys Asp Glu Ser Ala Glu Arg Ala
  1                   5                   10                   15

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Val Leu Gly Ser Met Leu Glu Asp Pro Glu Asn Ile Pro Leu Val Leu
                20                   25                   30

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Glu Tyr Leu Lys Glu Glu Asp Phe Cys Ile Asp Glu His Lys Leu Leu
        35                   40                   45

```

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Phe Arg Val Leu Thr Asn Leu Trp Ser Glu Tyr Gly Asn Lys Leu Asp
        50                   55                   60

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Phe Val Leu Ile Lys Asp His Leu Glu Lys Lys Asn Leu Leu Gln Lys
        65                   70                   75                   80

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Ile Pro Ile Asp Trp Leu Glu Glu Leu Tyr Glu Glu Ala Val Ser Pro

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	85		90		95
Asp Thr Leu Glu Glu Val Cys Lys Ile Val Lys Gln Arg Ser Ala Gln	100		105		110
Arg Ala Ile Ile Gln Leu Gly Ile Thr Ser Thr Gln Phe Tyr His Val	115		120		125
Lys Asp Val Ala Glu Glu Val Ile Glu Leu Ile Tyr Lys Phe Lys Ser	130		135		140
Ser Asp Arg Leu Val Thr Gly Leu Pro Ser Gly Phe Thr Glu Leu Asp	145		150		155
Leu Lys Thr Thr Gly Phe His Pro Gly Asp Leu Ile Ile Leu Ala Ala	165		170		175
Arg Pro Gly Met Gly Lys Thr Ala Phe Met Leu Ser Ile Ile Tyr Asn	180		185		190
Leu Ala Lys Asp Glu Gly Lys Pro Ser Ala Val Phe Ser Leu Glu Met	195		200		205
Ser Lys Glu Gln Leu Val Met Arg Leu Leu Ser Met Met Ser Glu Val	210		215		220
Pro Leu Phe Lys Ile Arg Ser Gly Ser Ile Ser Asn Glu Asp Leu Lys	225		230		235
Lys Leu Glu Ala Ser Ala Ile Glu Leu Ala Lys Tyr Asp Ile Tyr Leu	245		250		255
Asp Asp Thr Pro Ala Leu Thr Thr Thr Asp Leu Arg Ile Arg Ala Arg	260		265		270
Lys Leu Arg Lys Glu Lys Glu Val Glu Phe Val Ala Val Asp Tyr Leu	275		280		285
Gln Leu Leu Arg Pro Pro Val Arg Lys Ser Ser Arg Gln Glu Glu Val	290		295		300
Ala Glu Val Ser Arg Asn Leu Lys Ala Leu Ala Lys Glu Leu His Ile	305		310		315
Pro Val Met Ala Leu Ala Gln Leu Ser Arg Glu Val Glu Lys Arg Ser	325		330		335
Asp Lys Arg Pro Gln Leu Ala Asp Leu Arg Glu Ser Gly Gln Ile Glu					

340	345	350
Gln Asp Ala Asp Leu Ile Leu Phe Leu His Arg Pro Glu Tyr Tyr Lys		
355	360	365
Lys Lys Pro Asn Pro Glu Glu Gln Gly Ile Ala Glu Val Ile Ile Ala		
370	375	380
Lys Gln Arg Gln Gly Pro Thr Asp Ile Val Lys Leu Ala Phe Ile Lys		
385	390	395
400		
Glu Tyr Thr Lys Phe Ala Asn Leu Glu Ala Leu Pro Glu Gln Pro Pro		
405	410	415
Glu Glu Glu Glu Leu Ser Glu Ile Ile Glu Thr Gln Glu Asp Glu Gly		
420	425	430
Phe Glu Asp Ile Asp Phe		
435		

<210> 133
 <211> 1526
 <212> DNA
 <213> Aquifex aeolicus

<400> 133

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gatacaccct	cctttttacgt	gtctccaagt	aaacaaatat	tcaagtgttt	cggttgcggg	180
gtagggggag	acgcgataaa	gttcgtttcc	ctttacgagg	acatctccta	ttttgaagcc	240
gcccttgaac	tcgcaaaacg	ctacggaaaag	aaattagacc	ttgaaaagat	atcaaaagac	300
gaaaaggtat	acgtggctct	tgacagggtt	tgtgatttct	acagggaaaag	ccttctcaaa	360
aacagagagg	caagtgagta	cgtaaagagt	aggggaatag	accctaaagt	agcgagggaag	420
tttgatcttg	ggtacgcacc	ttccagtga	gcactcgtaa	aagtcttaaa	agagaacgat	480
cttttagagg	cttaccttga	aactaaaaac	ctcctttctc	ctacgaagg	tgtttacagg	540
gatctctttc	ttcggcgtgt	cgtgatcccg	ataaaggatc	cgaggggaag	agttataggt	600
ttcggtgga	ggaggatagt	agaggacaaa	tctcccaagt	acataaactc	tccagacagc	660
agggtattta	aaaaggggga	gaacttattc	ggtctttacg	aggcaaagga	gtatataaag	720
gaagaaggat	ttgcgatact	tgtggaagg	tactttgacc	ttttgagact	tttttccgag	780
ggaataagga	acgttggttg	acccctcgg	acagccctga	cccaaaatca	ggcaaacctc	840
ctttccaagt	tcacaaaaaa	ggtctacatc	ctttacgacg	gagatgatgc	gggaagaaag	900
gctatgaaaa	gtgccattcc	cctactcctc	agtgaggag	tggaagtta	tcccgtttac	960
ctccccgaag	gatacgatcc	cgacgagttt	ataaaggaat	tcgggaaaga	ggaattaaga	1020
agactgataa	acagctcagg	ggagctcttt	gaaacgctca	taaaaaccgc	aagggaac	1080
ttagaggaga	aaacgcgtga	gttcagggtat	tatctgggct	ttatttccga	tggaagtaagg	1140
cgctttgctc	tggcttcgga	gtttcacacc	aagtacaaag	ttcctatgga	aattttatta	1200
atgaaaattg	aaaaaaattc	tcaagaaaaa	gaaattaaac	tctccttta	ggaaaaaatc	1260

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 cctgagttaa aggaactcgc agttaacgcc ttaaaccggag aggagcattt acttccaaaa 1380
 gaagtctcgc agtaccaggt ggataacttg gagaaacttt ttaacaacat ccttagggat 1440
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<210> 134

<211> 498

<212> PRT

<213> Aquifex aeolicus

<400> 134

Met Ser Ser Asp Ile Asp Glu Leu Arg Arg Glu Ile Asp Ile Val Asp
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Val Ile Ser Glu Tyr Leu Asn Leu Glu Lys Val Gly Ser Asn Tyr Arg
 20 25 30

Thr Asn Cys Pro Phe His Pro Asp Asp Thr Pro Ser Phe Tyr Val Ser
 35 40 45

Pro Ser Lys Gln Ile Phe Lys Cys Phe Gly Cys Gly Val Gly Gly Asp
 50 55 60

Ala Ile Lys Phe Val Ser Leu Tyr Glu Asp Ile Ser Tyr Phe Glu Ala
 65 70 75 80

Ala Leu Glu Leu Ala Lys Arg Tyr Gly Lys Lys Leu Asp Leu Glu Lys
 85 90 95

Ile Ser Lys Asp Glu Lys Val Tyr Val Ala Leu Asp Arg Val Cys Asp
 100 105 110

Phe Tyr Arg Glu Ser Leu Leu Lys Asn Arg Glu Ala Ser Glu Tyr Val
 115 120 125

Lys Ser Arg Gly Ile Asp Pro Lys Val Ala Arg Lys Phe Asp Leu Gly
 130 135 140

Tyr Ala Pro Ser Ser Glu Ala Leu Val Lys Val Leu Lys Glu Asn Asp
 145 150 155 160

Leu Leu Glu Ala Tyr Leu Glu Thr Lys Asn Leu Leu Ser Pro Thr Lys
 165 170 175

Gly Val Tyr Arg Asp Leu Phe Leu Arg Arg Val Val Ile Pro Ile Lys
 180 185 190

Asp Pro Arg Gly Arg Val Ile Gly Phe Gly Gly Arg Arg Ile Val Glu
 195 200 205
 Asp Lys Ser Pro Lys Tyr Ile Asn Ser Pro Asp Ser Arg Val Phe Lys
 210 215 220
 Lys Gly Glu Asn Leu Phe Gly Leu Tyr Glu Ala Lys Glu Tyr Ile Lys
 225 230 235 240
 Glu Glu Gly Phe Ala Ile Leu Val Glu Gly Tyr Phe Asp Leu Leu Arg
 245 250 255
 Leu Phe Ser Glu Gly Ile Arg Asn Val Val Ala Pro Leu Gly Thr Ala
 260 265 270
 Leu Thr Gln Asn Gln Ala Asn Leu Leu Ser Lys Phe Thr Lys Lys Val
 275 280 285
 Tyr Ile Leu Tyr Asp Gly Asp Asp Ala Gly Arg Lys Ala Met Lys Ser
 290 295 300
 Ala Ile Pro Leu Leu Leu Ser Ala Gly Val Glu Val Tyr Pro Val Tyr
 305 310 315 320
 Leu Pro Glu Gly Tyr Asp Pro Asp Glu Phe Ile Lys Glu Phe Gly Lys
 325 330 335
 Glu Glu Leu Arg Arg Leu Ile Asn Ser Ser Gly Glu Leu Phe Glu Thr
 340 345 350
 Leu Ile Lys Thr Ala Arg Glu Asn Leu Glu Glu Lys Thr Arg Glu Phe
 355 360 365
 Arg Tyr Tyr Leu Gly Phe Ile Ser Asp Gly Val Arg Arg Phe Ala Leu
 370 375 380
 Ala Ser Glu Phe His Thr Lys Tyr Lys Val Pro Met Glu Ile Leu Leu
 385 390 395 400
 Met Lys Ile Glu Lys Asn Ser Gln Glu Lys Glu Ile Lys Leu Ser Phe
 405 410 415
 Lys Glu Lys Ile Phe Leu Lys Gly Leu Ile Glu Leu Lys Pro Lys Ile
 420 425 430
 Asp Leu Glu Val Leu Asn Leu Ser Pro Glu Leu Lys Glu Leu Ala Val
 435 440 445

Asn Ala Leu Asn Gly Glu Glu His Leu Leu Pro Lys Glu Val Leu Glu
 450 455 460

Tyr Gln Val Asp Asn Leu Glu Lys Leu Phe Asn Asn Ile Leu Arg Asp
 465 470 475 480

Leu Gln Lys Ser Gly Lys Lys Arg Lys Lys Arg Gly Leu Lys Asn Val
 485 490 495

Asn Thr

<210> 135

<211> 705

<212> DNA

<213> Aquifex aeolicus

<400> 135

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 atcccaaaga ggtactggaa cgccaactta gacacttacc accccaagaa cgtatcccag 180
 aacagggcac ttttgacgat aagggtcttc gtccacaact tcaatcccga ggaagggaaa 240
 gggcttacct ttgtaggatc tcttggagtc ggcaaaactc accttgcggt tgcaacatta 300
 aaagcgattt atgagaagaa gggaatcaga ggatacttct tcgatacgaa ggatctaata 360
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 aactcaccgg ttttggttct cgacgacctc ggttctgaga ggctcagtga ctggcagagg 480
 gaactcatct cttacataat cacttacagg tataacaacc ttaagagcac gataataacc 540
 acgaattact cactccagag ggaagaagag agtagcgtga ggataagtgc ggatcttgca 600
 agcagactcg gagaaaacgt agtttcaaaa atttacgaga tgaacgagtt gctcggtata 660
 aagggttccg acctcaggaa gtctaaaaag ctatcaaccc catct 705

<210> 136

<211> 235

<212> PRT

<213> Aquifex aeolicus

<400> 136

Met Gln Asp Thr Ala Thr Cys Ser Ile Cys Gln Gly Thr Gly Phe Val
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Lys Thr Glu Asp Asn Lys Val Arg Leu Cys Glu Cys Arg Phe Lys Lys
 20 25 30

Arg Asp Val Asn Arg Glu Leu Asn Ile Pro Lys Arg Tyr Trp Asn Ala
 35 40 45

Asn Leu Asp Thr Tyr His Pro Lys Asn Val Ser Gln Asn Arg Ala Leu
 50 55 60
 Leu Thr Ile Arg Val Phe Val His Asn Phe Asn Pro Glu Glu Gly Lys
 65 70 75 80
 Gly Leu Thr Phe Val Gly Ser Pro Gly Val Gly Lys Thr His Leu Ala
 85 90 95
 Val Ala Thr Leu Lys Ala Ile Tyr Glu Lys Lys Gly Ile Arg Gly Tyr
 100 105 110
 Phe Phe Asp Thr Lys Asp Leu Ile Phe Arg Leu Lys His Leu Met Asp
 115 120 125
 Glu Gly Lys Asp Thr Lys Phe Leu Lys Thr Val Leu Asn Ser Pro Val
 130 135 140
 Leu Val Leu Asp Asp Leu Gly Ser Glu Arg Leu Ser Asp Trp Gln Arg
 145 150 155 160
 Glu Leu Ile Ser Tyr Ile Ile Thr Tyr Arg Tyr Asn Asn Leu Lys Ser
 165 170 175
 Thr Ile Ile Thr Thr Asn Tyr Ser Leu Gln Arg Glu Glu Glu Ser Ser
 180 185 190
 Val Arg Ile Ser Ala Asp Leu Ala Ser Arg Leu Gly Glu Asn Val Val
 195 200 205
 Ser Lys Ile Tyr Glu Met Asn Glu Leu Leu Val Ile Lys Gly Ser Asp
 210 215 220
 Leu Arg Lys Ser Lys Lys Leu Ser Thr Pro Ser
 225 230 235

<210> 137
 <211> 4101
 <212> DNA
 <213> *Thermatoga maritima*

<400> 137
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 gtgcgtttac tggagaagaa gacgcggttt cgagtcacgc tgaacgggtg tcaaaaaagt 180
 aacggggatc taaggggaaa gatactttcc cttctcaacg gtaatgtgcc ttacataaaa 240

gatgttgttt	tcgaaggaaa	caggctgatt	ctgaaagtgc	ttggagattt	cgcgcgggac	300
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acagagatca	tgctggaggt	tgtggagcct	ccggaagatc	ttttgaaaaa	ggaagtacca	420
caaccagaaa	agagagaaga	accaaagggg	gaagaattga	agatcgagga	tgaaaaccac	480
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aaaaagacat	cgggtgaagg	caagatcttc	aaaatagaga	agatcgaggg	gaaaagaacg	600
gtccttctga	tttacctgac	agacggagaa	gattctctga	tctgcaaagt	cttcaacgac	660
gttgaaaagg	tcgaagggaa	agtatcgggt	ggagacgtga	tcgttgccac	aggagacctc	720
cttctcgaaa	acggggagcc	caccctttac	gtgaagggaa	tcacaaaact	tcccgaagcg	780
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<210> 138

<211> 1367

<212> PRT

<213> *Thermatoga maritima*

<400> 138

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Met Lys Lys Ile Glu Asn Leu Lys Trp Lys Asn Val Ser Phe Lys Ser
  1             5             10             15

```

```

Leu Glu Ile Asp Pro Asp Ala Gly Val Val Leu Val Ser Val Glu Lys
      20             25             30

```

```

Phe Ser Glu Glu Ile Glu Asp Leu Val Arg Leu Leu Glu Lys Lys Thr
      35             40             45

```

```

Arg Phe Arg Val Ile Val Asn Gly Val Gln Lys Ser Asn Gly Asp Leu
      50             55             60

```

```

Arg Gly Lys Ile Leu Ser Leu Leu Asn Gly Asn Val Pro Tyr Ile Lys
      65             70             75             80

```

```

Asp Val Val Phe Glu Gly Asn Arg Leu Ile Leu Lys Val Leu Gly Asp
      85             90             95

```

```

Phe Ala Arg Asp Arg Ile Ala Ser Lys Leu Arg Ser Thr Lys Lys Gln
      100            105            110

```

```

Leu Asp Glu Leu Leu Pro Pro Gly Thr Glu Ile Met Leu Glu Val Val
      115            120            125

```


Glu	Pro	Pro	Glu	Asp	Leu	Leu	Lys	Lys	Glu	Val	Pro	Gln	Pro	Glu	Lys	130	135	140	
Arg	Glu	Glu	Pro	Lys	Gly	Glu	Glu	Leu	Lys	Ile	Glu	Asp	Glu	Asn	His	145	150	155	160
Ile	Phe	Gly	Gln	Lys	Pro	Arg	Lys	Ile	Val	Phe	Thr	Pro	Ser	Lys	Ile	165	170	175	
Phe	Glu	Tyr	Asn	Lys	Lys	Thr	Ser	Val	Lys	Gly	Lys	Ile	Phe	Lys	Ile	180	185	190	
Glu	Lys	Ile	Glu	Gly	Lys	Arg	Thr	Val	Leu	Leu	Ile	Tyr	Leu	Thr	Asp	195	200	205	
Gly	Glu	Asp	Ser	Leu	Ile	Cys	Lys	Val	Phe	Asn	Asp	Val	Glu	Lys	Val	210	215	220	
Glu	Gly	Lys	Val	Ser	Val	Gly	Asp	Val	Ile	Val	Ala	Thr	Gly	Asp	Leu	225	230	235	240
Leu	Leu	Glu	Asn	Gly	Glu	Pro	Thr	Leu	Tyr	Val	Lys	Gly	Ile	Thr	Lys	245	250	255	
Leu	Pro	Glu	Ala	Lys	Arg	Met	Asp	Lys	Ser	Pro	Val	Lys	Arg	Val	Glu	260	265	270	
Leu	His	Ala	His	Thr	Lys	Phe	Ser	Asp	Gln	Asp	Ala	Ile	Thr	Asp	Val	275	280	285	
Asn	Glu	Tyr	Val	Lys	Arg	Ala	Lys	Glu	Trp	Gly	Phe	Pro	Ala	Ile	Ala	290	295	300	
Leu	Thr	Asp	His	Gly	Asn	Val	Gln	Ala	Ile	Pro	Tyr	Phe	Tyr	Asp	Ala	305	310	315	320
Ala	Lys	Glu	Ala	Gly	Ile	Lys	Pro	Ile	Phe	Gly	Ile	Glu	Ala	Tyr	Leu	325	330	335	
Val	Ser	Asp	Val	Glu	Pro	Val	Ile	Arg	Asn	Leu	Ser	Asp	Asp	Ser	Thr	340	345	350	
Phe	Gly	Asp	Ala	Thr	Phe	Val	Val	Leu	Asp	Phe	Glu	Thr	Thr	Gly	Leu	355	360	365	
Asp	Pro	Gln	Val	Asp	Glu	Ile	Ile	Glu	Ile	Gly	Ala	Val	Lys	Ile	Gln	370	375	380	

Gly	Gly	Gln	Ile	Val	Asp	Glu	Tyr	His	Thr	Leu	Ile	Lys	Pro	Ser	Arg	385	390	395	400
Glu	Ile	Ser	Arg	Lys	Ser	Ser	Glu	Ile	Thr	Gly	Ile	Thr	Gln	Glu	Met	405	410	415	
Leu	Glu	Asn	Lys	Arg	Ser	Ile	Glu	Glu	Val	Leu	Pro	Glu	Phe	Leu	Gly	420	425	430	
Phe	Leu	Glu	Asp	Ser	Ile	Ile	Val	Ala	His	Asn	Ala	Asn	Phe	Asp	Tyr	435	440	445	
Arg	Phe	Leu	Arg	Leu	Trp	Ile	Lys	Lys	Val	Met	Gly	Leu	Asp	Trp	Glu	450	455	460	
Arg	Pro	Tyr	Ile	Asp	Thr	Leu	Ala	Leu	Ala	Lys	Ser	Leu	Leu	Lys	Leu	465	470	475	480
Arg	Ser	Tyr	Ser	Leu	Asp	Ser	Val	Val	Glu	Lys	Leu	Gly	Leu	Gly	Pro	485	490	495	
Phe	Arg	His	His	Arg	Ala	Leu	Asp	Asp	Ala	Arg	Val	Thr	Ala	Gln	Val	500	505	510	
Phe	Leu	Arg	Phe	Val	Glu	Met	Met	Lys	Lys	Ile	Gly	Ile	Thr	Lys	Leu	515	520	525	
Ser	Glu	Met	Glu	Lys	Leu	Lys	Asp	Thr	Ile	Asp	Tyr	Thr	Ala	Leu	Lys	530	535	540	
Pro	Phe	His	Cys	Thr	Ile	Leu	Val	Gln	Asn	Lys	Lys	Gly	Leu	Lys	Asn	545	550	555	560
Leu	Tyr	Lys	Leu	Val	Ser	Asp	Ser	Tyr	Ile	Lys	Tyr	Phe	Tyr	Gly	Val	565	570	575	
Pro	Arg	Ile	Leu	Lys	Ser	Glu	Leu	Ile	Glu	Asn	Arg	Glu	Gly	Leu	Leu	580	585	590	
Val	Gly	Ser	Ala	Cys	Ile	Ser	Gly	Glu	Leu	Gly	Arg	Ala	Ala	Leu	Glu	595	600	605	
Gly	Ala	Ser	Asp	Ser	Glu	Leu	Glu	Glu	Ile	Ala	Lys	Phe	Tyr	Asp	Tyr	610	615	620	
Ile	Glu	Val	Met	Pro	Leu	Asp	Val	Ile	Ala	Glu	Asp	Glu	Glu	Asp	Leu	625	630	635	640

Asp	Arg	Glu	Arg	Leu	Lys	Glu	Val	Tyr	Arg	Lys	Leu	Tyr	Arg	Ile	Ala	645	650	655
Lys	Lys	Leu	Asn	Lys	Phe	Val	Val	Met	Thr	Gly	Asp	Val	His	Phe	Leu	660	665	670
Asp	Pro	Glu	Asp	Ala	Arg	Gly	Arg	Ala	Ala	Leu	Leu	Ala	Pro	Gln	Gly	675	680	685
Asn	Arg	Asn	Phe	Glu	Asn	Gln	Pro	Ala	Leu	Tyr	Leu	Arg	Thr	Thr	Glu	690	695	700
Glu	Met	Leu	Glu	Lys	Ala	Ile	Glu	Ile	Phe	Glu	Asp	Glu	Glu	Ile	Ala	705	710	715
Arg	Glu	Val	Val	Ile	Glu	Asn	Pro	Asn	Arg	Ile	Ala	Asp	Met	Ile	Glu	725	730	735
Glu	Val	Gln	Pro	Leu	Glu	Lys	Lys	Leu	His	Pro	Pro	Ile	Ile	Glu	Asn	740	745	750
Ala	Asp	Glu	Ile	Val	Arg	Asn	Leu	Thr	Met	Lys	Arg	Ala	Tyr	Glu	Ile	755	760	765
Tyr	Gly	Asp	Pro	Leu	Pro	Glu	Ile	Val	Gln	Lys	Arg	Val	Glu	Lys	Glu	770	775	780
Leu	Asn	Ala	Ile	Ile	Asn	His	Gly	Tyr	Ala	Val	Leu	Tyr	Leu	Ile	Ala	785	790	795
Gln	Glu	Leu	Val	Gln	Lys	Ser	Met	Ser	Asp	Gly	Tyr	Val	Val	Gly	Ser	805	810	815
Arg	Gly	Ser	Val	Gly	Ser	Ser	Leu	Val	Ala	Asn	Leu	Leu	Gly	Ile	Thr	820	825	830
Glu	Val	Asn	Pro	Leu	Pro	Pro	His	Tyr	Arg	Cys	Pro	Glu	Cys	Lys	Tyr	835	840	845
Phe	Glu	Val	Val	Glu	Asp	Asp	Arg	Tyr	Gly	Ala	Gly	Tyr	Asp	Leu	Pro	850	855	860
Asn	Lys	Asn	Cys	Pro	Arg	Cys	Gly	Ala	Pro	Leu	Arg	Lys	Asp	Gly	His	865	870	875
Gly	Ile	Pro	Phe	Glu	Thr	Phe	Met	Gly	Phe	Glu	Gly	Asp	Lys	Val	Pro	885	890	895

Asp Ile Asp Leu Asn Phe Ser Gly Glu Tyr Gln Glu Arg Ala His Arg
 900 905 910

Phe Val Glu Glu Leu Phe Gly Lys Asp His Val Tyr Arg Ala Gly Thr
 915 920 925

Ile Asn Thr Ile Ala Glu Arg Ser Ala Val Gly Tyr Val Arg Ser Tyr
 930 935 940

Glu Glu Lys Thr Gly Lys Lys Leu Arg Lys Ala Glu Met Glu Arg Leu
 945 950 955 960

Val Ser Met Ile Thr Gly Val Lys Arg Thr Thr Gly Gln His Pro Gly
 965 970 975

Gly Leu Met Ile Ile Pro Lys Asp Lys Glu Val Tyr Asp Phe Thr Pro
 980 985 990

Ile Gln Tyr Pro Ala Asn Asp Arg Asn Ala Gly Val Phe Thr Thr His
 995 1000 1005

Phe Ala Tyr Glu Thr Ile His Asp Asp Leu Val Lys Ile Asp Ala Leu
 1010 1015 1020

Gly His Asp Asp Pro Thr Phe Ile Lys Met Leu Lys Asp Leu Thr Gly
 1025 1030 1035 1040

Ile Asp Pro Met Thr Ile Pro Met Asp Asp Pro Asp Thr Leu Ala Ile
 1045 1050 1055

Phe Ser Ser Val Lys Pro Leu Gly Val Asp Pro Val Glu Leu Glu Ser
 1060 1065 1070

Asp Val Gly Thr Tyr Gly Ile Pro Glu Phe Gly Thr Glu Phe Val Arg
 1075 1080 1085

Gly Met Leu Val Glu Thr Arg Pro Lys Ser Phe Ala Glu Leu Val Arg
 1090 1095 1100

Ile Ser Gly Leu Ser His Gly Thr Asp Val Trp Leu Asn Asn Ala Arg
 1105 1110 1115 1120

Asp Trp Ile Asn Leu Gly Tyr Ala Lys Leu Ser Glu Val Ile Ser Cys
 1125 1130 1135

Arg Asp Asp Ile Met Asn Phe Leu Ile His Lys Gly Met Glu Pro Ser
 1140 1145 1150

Leu Ala Phe Lys Ile Met Glu Asn Val Arg Lys Gly Lys Gly Ile Thr
1155 1160 1165

Glu Glu Met Glu Ser Glu Met Arg Arg Leu Lys Val Pro Glu Trp Phe
1170 1175 1180

Ile Glu Ser Cys Lys Arg Ile Lys Tyr Leu Phe Pro Lys Ala His Ala
1185 1190 1195 1200

Val Ala Tyr Val Ser Met Ala Phe Arg Ile Ala Tyr Phe Lys Val His
1205 1210 1215

Tyr Pro Leu Gln Phe Tyr Ala Ala Tyr Phe Thr Ile Lys Gly Asp Gln
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Phe Asp Pro Val Leu Val Leu Arg Gly Lys Glu Ala Ile Lys Arg Arg
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Leu Arg Glu Leu Lys Ala Met Pro Ala Lys Asp Ala Gln Lys Lys Asn
1250 1255 1260

Glu Val Ser Val Leu Glu Val Ala Leu Glu Met Ile Leu Arg Gly Phe
1265 1270 1275 1280

Ser Phe Leu Pro Pro Asp Ile Phe Lys Ser Asp Ala Lys Lys Phe Leu
1285 1290 1295

Ile Glu Gly Asn Ser Leu Arg Ile Pro Phe Asn Lys Leu Pro Gly Leu
1300 1305 1310

Gly Asp Ser Val Ala Glu Ser Ile Ile Arg Ala Arg Glu Glu Lys Pro
1315 1320 1325

Phe Thr Ser Val Glu Asp Leu Met Lys Arg Thr Lys Val Asn Lys Asn
1330 1335 1340

His Ile Glu Leu Met Lys Ser Leu Gly Val Leu Gly Asp Leu Pro Glu
1345 1350 1355 1360

Thr Glu Gln Phe Thr Leu Phe
1365

<210> 139

<211> 567

<212> DNA

<213> *Thermatoga maritima*

<400> 139

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gtgctcgcca tgatatggaa cgacaccgtt ttttgcgtcg tagacacaga aaccacggga 60
accgatccct ttgccggaga ccgtagattt gaaatagccg ctgttcctgt cttcaagggg 120
aagatctaca gaaacaaagc gtttcaactct ctctggaatc ccagaataag aatccctgcg 180
ctgattcaga aagttcacgg tatcagcaac atggacatcg tggaagcgcc agacatggac 240
acagtttacg atcttttcag ggattacgtg aagggaacgg tgctcgtgtt tcacaacgcc 300
aacttcgacc tcacttttct ggatatgatg gcaaaggaaa cgggaaactt tccaataacg 360
aatccctaca tcgacacact cgatctttca gaagagatct ttggaaggcc tcattctctc 420
aaatggctct ccgaaagact tggaataaaa accacgatac ggcaccgtgc tttccagat 480
gccctggtga ccgcaagagt ttttgtgaag cttgttgaat ttcttggtga aaacagggtc 540
aacgaattca tacgtggaaa acggggg 567
```

<210> 140

<211> 189

<212> PRT

<213> *Thermatoga maritima*

<400> 140

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Met Leu Ala Met Ile Trp Asn Asp Thr Val Phe Cys Val Val Asp Thr
  1             5             10             15

Glu Thr Thr Gly Thr Asp Pro Phe Ala Gly Asp Arg Ile Val Glu Ile
      20             25             30

Ala Ala Val Pro Val Phe Lys Gly Lys Ile Tyr Arg Asn Lys Ala Phe
      35             40             45

His Ser Leu Val Asn Pro Arg Ile Arg Ile Pro Ala Leu Ile Gln Lys
      50             55             60

Val His Gly Ile Ser Asn Met Asp Ile Val Glu Ala Pro Asp Met Asp
      65             70             75             80

Thr Val Tyr Asp Leu Phe Arg Asp Tyr Val Lys Gly Thr Val Leu Val
      85             90             95

Phe His Asn Ala Asn Phe Asp Leu Thr Phe Leu Asp Met Met Ala Lys
      100            105            110

Glu Thr Gly Asn Phe Pro Ile Thr Asn Pro Tyr Ile Asp Thr Leu Asp
      115            120            125

Leu Ser Glu Glu Ile Phe Gly Arg Pro His Ser Leu Lys Trp Leu Ser
      130            135            140

Glu Arg Leu Gly Ile Lys Thr Thr Ile Arg His Arg Ala Leu Pro Asp
```

145	150	155	160
Ala Leu Val Thr	Ala Arg Val Phe Val Lys Leu Val Glu Phe Leu Gly		
	165	170	175
Glu Asn Arg Val Asn Glu Phe Ile Arg Gly Lys Arg Gly			
	180	185	

<210> 141
 <211> 1434
 <212> DNA
 <213> *Thermatoga maritima*

<400> 141

gtggaagttc	tttacaggaa	gtacaggcca	aagacttttt	ctgaggttgt	caatcaggat	60
catgtgaaga	aggcaataat	cgggtgctatt	cagaagaaca	gcgtggccca	cggatacata	120
ttcgccggtc	cgaggggaac	ggggaagact	actcttgcca	gaattctcgc	aaaatccctg	180
aactgtgaga	acagaaaagg	agttgaaccc	tgcaattcct	gcagagcctg	cagagagata	240
gacgagggaa	ccttcatgga	cgtgatagag	ctcgacgcgg	cctccaacag	aggaatagac	300
gagatcagaa	gaatcagaga	cgccgttgga	tacaggccga	tggaaggtaa	atacaaagtc	360
tacataatag	acgaagttca	catgctcacg	aaagaagcct	tcaacgcgct	cctcaaaaca	420
ctcgaagaac	ctccttccca	cgtcgtgttc	gtgctggcaa	cgacaaacct	tgagaagggt	480
cctcccacga	ttatctcgag	atgtcagggt	ttcgagttca	gaaacattcc	cgacgagctc	540
atcgaagaag	ggctccagga	agttgcggag	gctgaaggaa	tagagataga	cagggaaagct	600
ctgagcttca	tcgcaaaaag	agcctctgga	ggcttgagag	acgcgctcac	catgctcgag	660
caggtgtgga	agttctcgga	aggaaagata	gatctcgaga	cggtagacag	ggcgctcggg	720
ttgataccga	tacaggttgt	tcgcgattac	gtgaacgcta	tcttttctgg	tgatgtgaaa	780
agggtcttca	ccgttctcga	cgacgtctat	tacagcggga	aggactacga	ggtgctcatt	840
caggaagcag	tcgaggatct	ggtcgaagac	ctggaaaggg	agagaggggt	ttaccagggt	900
tcagcgaacg	atatagttca	ggttttcgaga	caacttctga	atcttctgag	agagataaag	960
ttcgccgaag	aaaaacgact	cgtctgtaaa	gtgggttcgg	cttacatagc	gacgaggttc	1020
tccaccacaa	acgttcagga	aaacgatgtc	agagaaaaaa	acgataattc	aaatgtacag	1080
cagaaagaag	agaagaaaga	aacggtgaag	gcaaaagaag	aaaaacagga	agacagcgag	1140
ttcgagaaac	gcttcaaaga	actcatggaa	gaactgaaag	aaaagggcga	tctctctatc	1200
tttgtcgtc	tcagcctctc	agaggtgcag	tttgacggag	aaaagggtgat	tatttctttt	1260
gattcatcga	aagctatgca	ttacgagttg	atgaagaaaa	aactgcctga	gctggaaaac	1320
attttttcta	gaaaactcgg	gaaaaaagta	gaagttgaac	ttcgactgat	gggaaaagaa	1380
gaaacaatcg	agaaggtttc	tcagaagatc	ctgagattgt	ttgaacagga	ggga	1434

<210> 142
 <211> 478
 <212> PRT
 <213> *Thermatoga maritima*

<400> 142

Met Glu Val Leu Tyr Arg Lys Tyr Arg Pro Lys Thr Phe Ser Glu Val

1	5	10	15
Val Asn Gln Asp His Val Lys Lys Ala Ile Ile Gly Ala Ile Gln Lys	20	25	30
Asn Ser Val Ala His Gly Tyr Ile Phe Ala Gly Pro Arg Gly Thr Gly	35	40	45
Lys Thr Thr Leu Ala Arg Ile Leu Ala Lys Ser Leu Asn Cys Glu Asn	50	55	60
Arg Lys Gly Val Glu Pro Cys Asn Ser Cys Arg Ala Cys Arg Glu Ile	65	70	75
Asp Glu Gly Thr Phe Met Asp Val Ile Glu Leu Asp Ala Ala Ser Asn	85	90	95
Arg Gly Ile Asp Glu Ile Arg Arg Ile Arg Asp Ala Val Gly Tyr Arg	100	105	110
Pro Met Glu Gly Lys Tyr Lys Val Tyr Ile Ile Asp Glu Val His Met	115	120	125
Leu Thr Lys Glu Ala Phe Asn Ala Leu Leu Lys Thr Leu Glu Glu Pro	130	135	140
Pro Ser His Val Val Phe Val Leu Ala Thr Thr Asn Leu Glu Lys Val	145	150	155
Pro Pro Thr Ile Ile Ser Arg Cys Gln Val Phe Glu Phe Arg Asn Ile	165	170	175
Pro Asp Glu Leu Ile Glu Lys Arg Leu Gln Glu Val Ala Glu Ala Glu	180	185	190
Gly Ile Glu Ile Asp Arg Glu Ala Leu Ser Phe Ile Ala Lys Arg Ala	195	200	205
Ser Gly Gly Leu Arg Asp Ala Leu Thr Met Leu Glu Gln Val Trp Lys	210	215	220
Phe Ser Glu Gly Lys Ile Asp Leu Glu Thr Val His Arg Ala Leu Gly	225	230	235
Leu Ile Pro Ile Gln Val Val Arg Asp Tyr Val Asn Ala Ile Phe Ser	245	250	255
Gly Asp Val Lys Arg Val Phe Thr Val Leu Asp Asp Val Tyr Tyr Ser			

260	265	270
Gly Lys Asp Tyr Glu Val Leu Ile Gln Glu Ala Val Glu Asp Leu Val		
275	280	285
Glu Asp Leu Glu Arg Glu Arg Gly Val Tyr Gln Val Ser Ala Asn Asp		
290	295	300
Ile Val Gln Val Ser Arg Gln Leu Leu Asn Leu Leu Arg Glu Ile Lys		
305	310	315
Phe Ala Glu Glu Lys Arg Leu Val Cys Lys Val Gly Ser Ala Tyr Ile		
325	330	335
Ala Thr Arg Phe Ser Thr Thr Asn Val Gln Glu Asn Asp Val Arg Glu		
340	345	350
Lys Asn Asp Asn Ser Asn Val Gln Gln Lys Glu Glu Lys Lys Glu Thr		
355	360	365
Val Lys Ala Lys Glu Glu Lys Gln Glu Asp Ser Glu Phe Glu Lys Arg		
370	375	380
Phe Lys Glu Leu Met Glu Glu Leu Lys Glu Lys Gly Asp Leu Ser Ile		
385	390	395
Phe Val Ala Leu Ser Leu Ser Glu Val Gln Phe Asp Gly Glu Lys Val		
405	410	415
Ile Ile Ser Phe Asp Ser Ser Lys Ala Met His Tyr Glu Leu Met Lys		
420	425	430
Lys Lys Leu Pro Glu Leu Glu Asn Ile Phe Ser Arg Lys Leu Gly Lys		
435	440	445
Lys Val Glu Val Glu Leu Arg Leu Met Gly Lys Glu Glu Thr Ile Glu		
450	455	460
Lys Val Ser Gln Lys Ile Leu Arg Leu Phe Glu Gln Glu Gly		
465	470	475

<210> 143

<211> 1098

<212> DNA

<213> *Thermatoga maritima*

<400> 143

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atgaaagtaa ccgtcacgac tcttgaattg aaagacaaaa taaccatcgc ctcaaaagcg 60
ctcgcaaaga aatccgtgaa acccattctt gctggatttc ttttcgaagt gaaagatgga 120
aattttctaca tctgcgcgac cgatctcgag accggagtca aagcaaccgt gaatgccgct 180
gaaatctccg gtgaggcacg ttttgtggta ccaggagatg tcattcagaa gatgggtcaag 240
gttctcccag atgagataac ggaactttct ttagaggggg atgctcttgt tataagttct 300
ggaagcaccg ttttcaggat caccaccatg cccgcggacg aatttccaga gataacgcct 360
gccgagtctg gaataacctt cgaagttgac acttcgctcc tcgaggaaat ggttgaaaag 420
gtcatcttcg ccgctgccaa agacgagttc atgcgaaatc tgaatggagt tttctgggaa 480
ctccacaaga atcttctcag gctggttgca agtgatggtt tcagacttgc acttgctgaa 540
gagcagatag aaaacgagga agaggcgagt ttcttgctct ctttgaagag catgaaagaa 600
gttcaaaacg tgctggacaa cacaacggag ccgactataa cggtgaggta cgatggaaga 660
agggttttctc tgctgcacaaa tgatgtagaa acggtgatga gagtggtcga cgctgaattt 720
cccgattaca aaagggtgat ccccgaaact ttcaaaacga aagtgggtgt ttccagaaaa 780
gaactcaggg aatctttgaa gaggggtgat gtgattgccg gcaaggggag cgagtcctgt 840
aagttcgaaa tagaagaaaa cgttatgaga cttgtgagca agagcccga ttatggagaa 900
gtggtcgatg aagttgaagt tcaaaaagaa ggggaagatc tcgtgatcgc tttcaaccgc 960
aagttcatcg aggacgtttt gaagcacatt gagactgaag aaatcgaaat gaacttcgtt 1020
gattctacca gtccatgtca gataaatcca ctcgatattt ctggatacct ttacatagtg 1080
atgcccataca gactggca 1098

```

<210> 144

<211> 366

<212> PRT

<213> *Thermatoga maritima*

<400> 144

```

Met Lys Val Thr Val Thr Thr Leu Glu Leu Lys Asp Lys Ile Thr Ile
  1                      5                      10                      15

```

```

Ala Ser Lys Ala Leu Ala Lys Lys Ser Val Lys Pro Ile Leu Ala Gly
      20                      25                      30

```

```

Phe Leu Phe Glu Val Lys Asp Gly Asn Phe Tyr Ile Cys Ala Thr Asp
    35                      40                      45

```

```

Leu Glu Thr Gly Val Lys Ala Thr Val Asn Ala Ala Glu Ile Ser Gly
    50                      55                      60

```

```

Glu Ala Arg Phe Val Val Pro Gly Asp Val Ile Gln Lys Met Val Lys
    65                      70                      75                      80

```

```

Val Leu Pro Asp Glu Ile Thr Glu Leu Ser Leu Glu Gly Asp Ala Leu
      85                      90                      95

```

```

Val Ile Ser Ser Gly Ser Thr Val Phe Arg Ile Thr Thr Met Pro Ala
    100                      105                      110

```

Asp	Glu	Phe	Pro	Glu	Ile	Thr	Pro	Ala	Glu	Ser	Gly	Ile	Thr	Phe	Glu	115	120	125	
Val	Asp	Thr	Ser	Leu	Leu	Glu	Glu	Met	Val	Glu	Lys	Val	Ile	Phe	Ala	130	135	140	
Ala	Ala	Lys	Asp	Glu	Phe	Met	Arg	Asn	Leu	Asn	Gly	Val	Phe	Trp	Glu	145	150	155	160
Leu	His	Lys	Asn	Leu	Leu	Arg	Leu	Val	Ala	Ser	Asp	Gly	Phe	Arg	Leu	165	170	175	
Ala	Leu	Ala	Glu	Glu	Gln	Ile	Glu	Asn	Glu	Glu	Glu	Ala	Ser	Phe	Leu	180	185	190	
Leu	Ser	Leu	Lys	Ser	Met	Lys	Glu	Val	Gln	Asn	Val	Leu	Asp	Asn	Thr	195	200	205	
Thr	Glu	Pro	Thr	Ile	Thr	Val	Arg	Tyr	Asp	Gly	Arg	Arg	Val	Ser	Leu	210	215	220	
Ser	Thr	Asn	Asp	Val	Glu	Thr	Val	Met	Arg	Val	Val	Asp	Ala	Glu	Phe	225	230	235	240
Pro	Asp	Tyr	Lys	Arg	Val	Ile	Pro	Glu	Thr	Phe	Lys	Thr	Lys	Val	Val	245	250	255	
Val	Ser	Arg	Lys	Glu	Leu	Arg	Glu	Ser	Leu	Lys	Arg	Val	Met	Val	Ile	260	265	270	
Ala	Ser	Lys	Gly	Ser	Glu	Ser	Val	Lys	Phe	Glu	Ile	Glu	Glu	Asn	Val	275	280	285	
Met	Arg	Leu	Val	Ser	Lys	Ser	Pro	Asp	Tyr	Gly	Glu	Val	Val	Asp	Glu	290	295	300	
Val	Glu	Val	Gln	Lys	Glu	Gly	Glu	Asp	Leu	Val	Ile	Ala	Phe	Asn	Pro	305	310	315	320
Lys	Phe	Ile	Glu	Asp	Val	Leu	Lys	His	Ile	Glu	Thr	Glu	Glu	Ile	Glu	325	330	335	
Met	Asn	Phe	Val	Asp	Ser	Thr	Ser	Pro	Cys	Gln	Ile	Asn	Pro	Leu	Asp	340	345	350	
Ile	Ser	Gly	Tyr	Leu	Tyr	Ile	Val	Met	Pro	Ile	Arg	Leu	Ala			355	360	365	

<210> 145
 <211> 972
 <212> DNA
 <213> *Thermatoga maritima*

<400> 145
 atgccagtca cgtttctcac aggtactgca gaaactcaga aggaagaatt gataaagaaa 60
 ctctgaagg atggtaacgt ggagtacata aggatccatc cggaggatcc cgacaagatc 120
 gatttcataa ggtctttact caggacaaag acgatctttt ccaacaagac gatcattgac 180
 atcgtcaatt tcgatgagtg gaaagcacag gagcagaagc gtctcgttga acttttgaaa 240
 aacgtaccgg aagacgttca tatcttcatc cgttctcaaa aaacagggtg aaagggagta 300
 gcgctggagc ttccgaagcc atgggaaacg gacaagtggc ttgagtggat agaaaagcgc 360
 ttcagggaga atggtttgct catcgataaa gatgcccttc agctgttttt ctccaagggt 420
 ggaacgaacg acctgatcat agaaagggag attgaaaaac tgaaagctta ttccgaggac 480
 agaaagataa cggtagaaga cgtggaagag gtcgttttta cctatcagac tccgggatac 540
 gatgattttt gctttgctgt ttccgaagga aaaaggaagc tcgctcactc tcttctgtcg 600
 cagctgtgga aaaccacaga gtccgtggtg attgccactg tccttgcgaa tcacttcttg 660
 gatctcttca aaatcctcgt tcttgtagaca aagaaaagat actacacctg gcctgatgtg 720
 tccaggggtg ccaaagagct gggaaattccc gttcctcgtg tggctcgttt cctcggtttc 780
 tcctttaaga cctggaaatt caaggtgatg aaccacctcc tctactacga tgtgaagaag 840
 gttagaaaaga tactgagggg tctctacgat ctggacagag ccgtgaaaag cgaagaagat 900
 ccaaaaccgt tcttccacga gttcatagaa gaggtggcac tggatgtata ttctcttcag 960
 agagatgaag aa 972

<210> 146
 <211> 324
 <212> PRT
 <213> *Thermatoga maritima*

<400> 146
 Met Pro Val Thr Phe Leu Thr Gly Thr Ala Glu Thr Gln Lys Glu Glu
 1 5 10 15
 Leu Ile Lys Lys Leu Leu Lys Asp Gly Asn Val Glu Tyr Ile Arg Ile
 20 25 30
 His Pro Glu Asp Pro Asp Lys Ile Asp Phe Ile Arg Ser Leu Leu Arg
 35 40 45
 Thr Lys Thr Ile Phe Ser Asn Lys Thr Ile Ile Asp Ile Val Asn Phe
 50 55 60
 Asp Glu Trp Lys Ala Gln Glu Gln Lys Arg Leu Val Glu Leu Leu Lys
 65 70 75 80
 Asn Val Pro Glu Asp Val His Ile Phe Ile Arg Ser Gln Lys Thr Gly

85					90					95						
Gly	Lys	Gly	Val	Ala	Leu	Glu	Leu	Pro	Lys	Pro	Trp	Glu	Thr	Asp	Lys	
100					105					110						
Trp	Leu	Glu	Trp	Ile	Glu	Lys	Arg	Phe	Arg	Glu	Asn	Gly	Leu	Leu	Ile	
115					120					125						
Asp	Lys	Asp	Ala	Leu	Gln	Leu	Phe	Phe	Ser	Lys	Val	Gly	Thr	Asn	Asp	
130					135					140						
Leu	Ile	Ile	Glu	Arg	Glu	Ile	Glu	Lys	Leu	Lys	Ala	Tyr	Ser	Glu	Asp	
145					150					155					160	
Arg	Lys	Ile	Thr	Val	Glu	Asp	Val	Glu	Glu	Val	Val	Phe	Thr	Tyr	Gln	
165					170					175						
Thr	Pro	Gly	Tyr	Asp	Asp	Phe	Cys	Phe	Ala	Val	Ser	Glu	Gly	Lys	Arg	
180					185					190						
Lys	Leu	Ala	His	Ser	Leu	Leu	Ser	Gln	Leu	Trp	Lys	Thr	Thr	Glu	Ser	
195					200					205						
Val	Val	Ile	Ala	Thr	Val	Leu	Ala	Asn	His	Phe	Leu	Asp	Leu	Phe	Lys	
210					215					220						
Ile	Leu	Val	Leu	Val	Thr	Lys	Lys	Arg	Tyr	Tyr	Thr	Trp	Pro	Asp	Val	
225					230					235					240	
Ser	Arg	Val	Ser	Lys	Glu	Leu	Gly	Ile	Pro	Val	Pro	Arg	Val	Ala	Arg	
245					250					255						
Phe	Leu	Gly	Phe	Ser	Phe	Lys	Thr	Trp	Lys	Phe	Lys	Val	Met	Asn	His	
260					265					270						
Leu	Leu	Tyr	Tyr	Asp	Val	Lys	Lys	Val	Arg	Lys	Ile	Leu	Arg	Asp	Leu	
275					280					285						
Tyr	Asp	Leu	Asp	Arg	Ala	Val	Lys	Ser	Glu	Glu	Asp	Pro	Lys	Pro	Phe	
290					295					300						
Phe	His	Glu	Phe	Ile	Glu	Glu	Val	Ala	Leu	Asp	Val	Tyr	Ser	Leu	Gln	
305					310					315					320	
Arg	Asp	Glu	Glu													

<210> 147
 <211> 936
 <212> DNA
 <213> *Thermatoga maritima*

<400> 147
 atgaacgatt tgatcagaaa gtacgctaaa gatcaactgg aaactttgaa aaggatcata 60
 gaaaagtctg aaggaatatc catcctcata aatggagaag atctctcgta tccgagagaa 120
 gtatcccctg aacttcccga gtacgtggag aaatttcccc cgaaggcctc ggatgttctg 180
 gagatagatc ccgaggggga gaacataggc atagacgaca tcagaacgat aaaggacttc 240
 ctgaactaca gccccgagct ctacacgaga aagtacgtga tagtccacga ctgtgaaaga 300
 atgaccagc aggcggcgaa cgcgtttctg aaggcccttg aagaaccacc agaatacgct 360
 gtgatcggtc tgaacactcg ccgctggcat tatctactgc cgacgataaa gagccgagt 420
 ttcagagtgg ttgtgaacgt tccaaaggag ttcagagatc tcgtgaaaga gaaaatagga 480
 gatctctggg aggaacttcc acttcttgag agagacttca aaacggctct cgaagcctac 540
 aaacttggtg cggaaaaact ttctggattg atggaaagtc tcaaagtttt ggagacggaa 600
 aaactcttga aaaaggtcct ttcaaaaggc ctcgaagggt atctcgcatg tagggagctc 660
 ctggagagat tttcaaaggt ggaatcgaag gaattctttg cgctttttga tcaggtgact 720
 aacacgataa caggaaaaga cgcgtttctt ttgatccaga gactgacaag aatcattctc 780
 cacgaaaaca catgggaaag cgttgaagat caaaaaagcg tgtctttcct cgattcaatt 840
 ctcagggtga agatagcgaa tctgaacaac aaactcactc tgatgaacat cctcgcgata 900
 cacagagaga gaaagagagg tgtcaacgct tggagc 936

<210> 148
 <211> 311
 <212> PRT
 <213> *Thermatoga maritima*

<400> 148
 Met Asn Asp Leu Ile Arg Lys Tyr Ala Lys Asp Gln Leu Glu Thr Leu
 1 5 10 15
 Lys Arg Ile Ile Glu Lys Ser Glu Gly Ile Ser Ile Leu Ile Asn Gly
 20 25 30
 Glu Asp Leu Ser Tyr Pro Arg Glu Val Ser Leu Glu Leu Pro Glu Tyr
 35 40 45
 Val Glu Lys Phe Pro Pro Lys Ala Ser Asp Val Leu Glu Ile Asp Pro
 50 55 60
 Glu Gly Glu Asn Ile Gly Ile Asp Asp Ile Arg Thr Ile Lys Asp Phe
 65 70 75 80
 Leu Asn Tyr Ser Pro Glu Leu Tyr Thr Arg Lys Tyr Val Ile Val His
 85 90 95

Asp Cys Glu Arg Met Thr Gln Gln Ala Ala Asn Ala Phe Leu Lys Ala
 100 105 110
 Leu Glu Glu Pro Pro Glu Tyr Ala Val Ile Val Leu Asn Thr Arg Arg
 115 120 125
 Trp His Tyr Leu Leu Pro Thr Ile Lys Ser Arg Val Phe Arg Val Val
 130 135 140
 Val Asn Val Pro Lys Glu Phe Arg Asp Leu Val Lys Glu Lys Ile Gly
 145 150 155 160
 Asp Leu Trp Glu Glu Leu Pro Leu Leu Glu Arg Asp Phe Lys Thr Ala
 165 170 175
 Leu Glu Ala Tyr Lys Leu Gly Ala Glu Lys Leu Ser Gly Leu Met Glu
 180 185 190
 Ser Leu Lys Val Leu Glu Thr Glu Lys Leu Leu Lys Lys Val Leu Ser
 195 200 205
 Lys Gly Leu Glu Gly Tyr Leu Ala Cys Arg Glu Leu Leu Glu Arg Phe
 210 215 220
 Ser Lys Val Glu Ser Lys Glu Phe Phe Ala Leu Phe Asp Gln Val Thr
 225 230 235 240
 Asn Thr Ile Thr Gly Lys Asp Ala Phe Leu Leu Ile Gln Arg Leu Thr
 245 250 255
 Arg Ile Ile Leu His Glu Asn Thr Trp Glu Ser Val Glu Asp Lys Ser
 260 265 270
 Val Ser Phe Leu Asp Ser Ile Leu Arg Val Lys Ile Ala Asn Leu Asn
 275 280 285
 Asn Lys Leu Thr Leu Met Asn Ile Leu Ala Ile His Arg Glu Arg Lys
 290 295 300
 Arg Gly Val Asn Ala Trp Ser
 305 310

<210> 149

<211> 423

<212> DNA

<213> *Thermatoga maritima*

<400> 149

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atgtctttct tcaacaagat catactcata ggaagactcg tgagagatcc cgaagagaga 60
tacacgtca gcggaactcc agtcaccacc ttcaccatag cgggtggacag ggttcccaga 120
aagaacgcgc cggacgacgc tcaaacgact gatttcttca ggatcgtcac ctttggaaga 180
ctggcagagt tcgctagaac ctatctcacc aaaggaaggc tcgttctcgt cgaaggtgaa 240
atgagaatga gaagatggga aacacccact ggagaaaaga gggatatctcc ggagggttgtc 300
gcaaacgttg ttagattcat ggacagaaaa cctgctgaaa cagttagcga gactgaagag 360
gagctggaaa taccggaaga agacttttcc agcgatacct tcagtgaaga tgaaccacca 420
ttt 423
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<210> 150

<211> 141

<212> PRT

<213> *Thermatoga maritima*

<400> 150

```
Met Ser Phe Phe Asn Lys Ile Ile Leu Ile Gly Arg Leu Val Arg Asp
  1             5             10             15

Pro Glu Glu Arg Tyr Thr Leu Ser Gly Thr Pro Val Thr Thr Phe Thr
      20             25             30

Ile Ala Val Asp Arg Val Pro Arg Lys Asn Ala Pro Asp Asp Ala Gln
      35             40             45

Thr Thr Asp Phe Phe Arg Ile Val Thr Phe Gly Arg Leu Ala Glu Phe
      50             55             60

Ala Arg Thr Tyr Leu Thr Lys Gly Arg Leu Val Leu Val Glu Gly Glu
      65             70             75             80

Met Arg Met Arg Arg Trp Glu Thr Pro Thr Gly Glu Lys Arg Val Ser
      85             90             95

Pro Glu Val Val Ala Asn Val Val Arg Phe Met Asp Arg Lys Pro Ala
      100            105            110

Glu Thr Val Ser Glu Thr Glu Glu Glu Leu Glu Ile Pro Glu Glu Asp
      115            120            125

Phe Ser Ser Asp Thr Phe Ser Glu Asp Glu Pro Pro Phe
      130            135            140
```

<210> 151

<211> 1353

<212> DNA

<213> *Thermatoga maritima*

<400> 151

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atgcgtgttc ccccgacaaa cttagaggcc gaagttgctg tgctcggaag catattgata 60
gatccgtcgg taataaacga cgttcttgaa attttgagcc acgaagattt ctatctgaaa 120
aaacaccaac acatcttcag agcgatggaa gagctttacg acgaaggaaa accggtggac 180
gtggtttccg tctgtgacaa gcttcaaagc atgggaaaaac tcgaggaagt aggtggagat 240
ctggaagtgg cccagctcgc tgaggctgtg cccagttctg cacacgcact tctactacgcg 300
gagatcgtca aggaaaaatc cattctgagg aaactcattg agatctccag aaaaatctca 360
gaaagtgcct acatggaaga agatgtggag atcctgctcg acaacgcaga aaagatgata 420
ttcgagatct cagagatgaa aacgacaaaa tctacgatac atctgagagg catcatgcac 480
cgggtgtttg aaaacctgga gaacttcagg gaaagagcca accttataga acccggtgtg 540
ctcataacgg gactaccaac gggattcaaa agtctggaca aacagaccac aggggtccac 600
agctccgatac tggatgataat agcagcgaga ccctccatgg gaaaaacctc ctctgcactc 660
tcaatagcga ggaacatggc tgtcaatttc gaaatccccg tcggaatatt cagtctcgag 720
atgtccaagg aacagctcgc tcaaagacta ctacagcatg agtccggtgt ggatctttac 780
agcatcagaa caggatacct ggatcaggag aagtgggaaa gactcacaat agcggcttct 840
aaactctaca aagcaccatc agttgtggac gatgagtcac tctctgatcc gcgatcggtg 900
agggcaaaaag cgagaaggat gaaaaaagaa tacgatgtaa aagccatttt tgctcgactat 960
ctccagctca tgcacctgaa aggaagaaaa gaaagcagac agcaggagat atccgagatac 1020
tcgagatctc tgaagctcct tgcgagggaa ctgcacatag tggatgatac gctttcacag 1080
ctttcgaggg ccgtagaaca gagagaagac aaaagaccga ggctgagtga cctcagggaa 1140
tccggtgcga tagaacagga cgcagacaca gtcattctca tctacaggga ggaatattac 1200
aggagcaaaa aatccaaaga ggaaagcaag cttcacgaac ctacagaaac tgaaatcata 1260
ataggtaaac agagaaacgg tcccggttga acgatcactc tgatcttoga cccagaagac 1320
gttacgttcc atgaagtcga tgtggtgcat tca 1353
```

<210> 152

<211> 451

<212> PRT

<213> *Thermatoga maritima*

<400> 152

```
Met Arg Val Pro Pro His Asn Leu Glu Ala Glu Val Ala Val Leu Gly
  1             5             10             15
```

```
Ser Ile Leu Ile Asp Pro Ser Val Ile Asn Asp Val Leu Glu Ile Leu
      20             25             30
```

```
Ser His Glu Asp Phe Tyr Leu Lys Lys His Gln His Ile Phe Arg Ala
      35             40             45
```

```
Met Glu Glu Leu Tyr Asp Glu Gly Lys Pro Val Asp Val Val Ser Val
      50             55             60
```

```
Cys Asp Lys Leu Gln Ser Met Gly Lys Leu Glu Glu Val Gly Gly Asp
      65             70             75             80
```

Leu Glu Val Ala Gln Leu Ala Glu Ala Val Pro Ser Ser Ala His Ala
 85 90 95

Leu His Tyr Ala Glu Ile Val Lys Glu Lys Ser Ile Leu Arg Lys Leu
 100 105 110

Ile Glu Ile Ser Arg Lys Ile Ser Glu Ser Ala Tyr Met Glu Glu Asp
 115 120 125

Val Glu Ile Leu Leu Asp Asn Ala Glu Lys Met Ile Phe Glu Ile Ser
 130 135 140

Glu Met Lys Thr Thr Lys Ser Tyr Asp His Leu Arg Gly Ile Met His
 145 150 155 160

Arg Val Phe Glu Asn Leu Glu Asn Phe Arg Glu Arg Ala Asn Leu Ile
 165 170 175

Glu Pro Gly Val Leu Ile Thr Gly Leu Pro Thr Gly Phe Lys Ser Leu
 180 185 190

Asp Lys Gln Thr Thr Gly Phe His Ser Ser Asp Leu Val Ile Ile Ala
 195 200 205

Ala Arg Pro Ser Met Gly Lys Thr Ser Phe Ala Leu Ser Ile Ala Arg
 210 215 220

Asn Met Ala Val Asn Phe Glu Ile Pro Val Gly Ile Phe Ser Leu Glu
 225 230 235 240

Met Ser Lys Glu Gln Leu Ala Gln Arg Leu Leu Ser Met Glu Ser Gly
 245 250 255

Val Asp Leu Tyr Ser Ile Arg Thr Gly Tyr Leu Asp Gln Glu Lys Trp
 260 265 270

Glu Arg Leu Thr Ile Ala Ala Ser Lys Leu Tyr Lys Ala Pro Ile Val
 275 280 285

Val Asp Asp Glu Ser Leu Leu Asp Pro Arg Ser Leu Arg Ala Lys Ala
 290 295 300

Arg Arg Met Lys Lys Glu Tyr Asp Val Lys Ala Ile Phe Val Asp Tyr
 305 310 315 320

Leu Gln Leu Met His Leu Lys Gly Arg Lys Glu Ser Arg Gln Gln Glu
 325 330 335

Ile Ser Glu Ile Ser Arg Ser Leu Lys Leu Leu Ala Arg Glu Leu Asp
340 345 350

Ile Val Val Ile Ala Leu Ser Gln Leu Ser Arg Ala Val Glu Gln Arg
355 360 365

Glu Asp Lys Arg Pro Arg Leu Ser Asp Leu Arg Glu Ser Gly Ala Ile
370 375 380

Glu Gln Asp Ala Asp Thr Val Ile Phe Ile Tyr Arg Glu Glu Tyr Tyr
385 390 395 400

Arg Ser Lys Lys Ser Lys Glu Glu Ser Lys Leu His Glu Pro His Glu
405 410 415

Ala Glu Ile Ile Ile Gly Lys Gln Arg Asn Gly Pro Val Gly Thr Ile
420 425 430

Thr Leu Ile Phe Asp Pro Arg Thr Val Thr Phe His Glu Val Asp Val
435 440 445

Val His Ser
450

<210> 153

<211> 1695

<212> DNA

<213> *Thermatoga maritima*

<400> 153

```
gtgattcctc gagaggtcat cgaggaaata aaagaaaagg ttgacatcgt agaggtcatt 60
tccgagtacg tgaatcttac ccgggtaggt tcctcctaca gggctctctg tccctttcat 120
tcagaaacca atccttcttt ctacgttcat ccgggtttga agatatacca ttgtttcggc 180
tgcggtgcga gtggagacgt catcaaattt cttcaagaaa tggaagggat cagtttccag 240
gaagcgctgg aaagacttgc caaaagagct gggattgatc tttctctcta cagaacagaa 300
gggacttctg aatacggaaa atacattcgt ttgtacgaag aaacgtggaa aaggtacgtc 360
aaagagctgg agaaatcgaa agaggcaaaa gactatttaa aaagcagagg cttctctgaa 420
gaagatatag caaagttcgg ctttggttac gtccccaaga gatccagcat ctctatagaa 480
gttgacagaag gcatgaacat aacactggaa gaacttgtca gatacggtat cgcgctgaaa 540
aagggtgatc gattcgttga tagattcgaa ggaagaatcg ttgttccaat aaagaacgac 600
agtggtcata ttgtggcttt tgggtggcgt gctctcggca acgaagaacc gaagtatttg 660
aactctccag agaccaggta ttttctgaag aagaagaccc ttttctctt cgatgaggcg 720
aaaaaagtgg caaaagaggt tggttttttc gtcatcaccg aaggctactt cgacgcgctc 780
gcattcagaa aggatggaat accaacggcg gtcgctgttc ttggggcgag tctttcaaga 840
gaggcgattc taaaactttc ggcgtattcg aaaaacgtca tactgtgttt cgataatgac 900
aaagcaggct tcagagccac tctcaaatcc ctcgaggatc tcctagacta cgaattcaac 960
```

```

gtgcttgtgg caacccctc tccttacaaa gacccagatg aactctttca gaaagaagga 1020
gaagggttcat tgaaaaagat gctgaaaaac tcgcgttcgt tcgaatattt tctggtgacg 1080
gctggtgagg tcttctttga caggaacagc cccgcgggtg tgagatccta cttttctttc 1140
ctcaaagggtt ggggtccaaaa gatgagaagg aaaggatatt tgaaacacat agaaaatctc 1200
gtgaatgagg tttcatcttc tctccagata ccagaaaacc agattttgaa cttttttgaa 1260
agcgacaggt ctaacactat gcctgttcat gagaccaagt cgtcaaagg tttacgatgag 1320
gggagaggac tggcttattt gtttttgaac tacgaggatt tgagggaaaa gattctggaa 1380
ctggacttag aggtactgga agataaaaaac gcgagggagt ttttcaagag agtctcactg 1440
ggagaagatt tgaacaaagt catagaaaac ttcccaaaag agctgaaaga ctggattttt 1500
gagacaatag aaagcattcc tcctccaaag gatcccgaga aattcctcgg tgacctctcc 1560
gaaaagttga aaatccgacg gatagagaga cgtatcgcag aaatagatga tatgataaag 1620
aaagcttcaa acgatgaaga aaggcgtctt cttctctcta tgaaagtgga tctcctcaga 1680
aaaataaaga ggagg                                     1695

```

<210> 154

<211> 565

<212> PRT

<213> *Thermatoga maritima*

<400> 154

```

Met Ile Pro Arg Glu Val Ile Glu Glu Ile Lys Glu Lys Val Asp Ile
  1             5             10             15

Val Glu Val Ile Ser Glu Tyr Val Asn Leu Thr Arg Val Gly Ser Ser
          20             25             30

Tyr Arg Ala Leu Cys Pro Phe His Ser Glu Thr Asn Pro Ser Phe Tyr
      35             40             45

Val His Pro Gly Leu Lys Ile Tyr His Cys Phe Gly Cys Gly Ala Ser
      50             55             60

Gly Asp Val Ile Lys Phe Leu Gln Glu Met Glu Gly Ile Ser Phe Gln
      65             70             75             80

Glu Ala Leu Glu Arg Leu Ala Lys Arg Ala Gly Ile Asp Leu Ser Leu
          85             90             95

Tyr Arg Thr Glu Gly Thr Ser Glu Tyr Gly Lys Tyr Ile Arg Leu Tyr
      100             105             110

Glu Glu Thr Trp Lys Arg Tyr Val Lys Glu Leu Glu Lys Ser Lys Glu
      115             120             125

Ala Lys Asp Tyr Leu Lys Ser Arg Gly Phe Ser Glu Glu Asp Ile Ala
      130             135             140

```

Lys Phe Gly Phe Gly Tyr Val Pro Lys Arg Ser Ser Ile Ser Ile Glu
 145 150 155 160
 Val Ala Glu Gly Met Asn Ile Thr Leu Glu Glu Leu Val Arg Tyr Gly
 165 170 175
 Ile Ala Leu Lys Lys Gly Asp Arg Phe Val Asp Arg Phe Glu Gly Arg
 180 185 190
 Ile Val Val Pro Ile Lys Asn Asp Ser Gly His Ile Val Ala Phe Gly
 195 200 205
 Gly Arg Ala Leu Gly Asn Glu Glu Pro Lys Tyr Leu Asn Ser Pro Glu
 210 215 220
 Thr Arg Tyr Phe Ser Lys Lys Lys Thr Leu Phe Leu Phe Asp Glu Ala
 225 230 235 240
 Lys Lys Val Ala Lys Glu Val Gly Phe Phe Val Ile Thr Glu Gly Tyr
 245 250 255
 Phe Asp Ala Leu Ala Phe Arg Lys Asp Gly Ile Pro Thr Ala Val Ala
 260 265 270
 Val Leu Gly Ala Ser Leu Ser Arg Glu Ala Ile Leu Lys Leu Ser Ala
 275 280 285
 Tyr Ser Lys Asn Val Ile Leu Cys Phe Asp Asn Asp Lys Ala Gly Phe
 290 295 300
 Arg Ala Thr Leu Lys Ser Leu Glu Asp Leu Leu Asp Tyr Glu Phe Asn
 305 310 315 320
 Val Leu Val Ala Thr Pro Ser Pro Tyr Lys Asp Pro Asp Glu Leu Phe
 325 330 335
 Gln Lys Glu Gly Glu Gly Ser Leu Lys Lys Met Leu Lys Asn Ser Arg
 340 345 350
 Ser Phe Glu Tyr Phe Leu Val Thr Ala Gly Glu Val Phe Phe Asp Arg
 355 360 365
 Asn Ser Pro Ala Gly Val Arg Ser Tyr Leu Ser Phe Leu Lys Gly Trp
 370 375 380
 Val Gln Lys Met Arg Arg Lys Gly Tyr Leu Lys His Ile Glu Asn Leu
 385 390 395 400

Val Asn Glu Val Ser Ser Ser Leu Gln Ile Pro Glu Asn Gln Ile Leu
 405 410 415
 Asn Phe Phe Glu Ser Asp Arg Ser Asn Thr Met Pro Val His Glu Thr
 420 425 430
 Lys Ser Ser Lys Val Tyr Asp Glu Gly Arg Gly Leu Ala Tyr Leu Phe
 435 440 445
 Leu Asn Tyr Glu Asp Leu Arg Glu Lys Ile Leu Glu Leu Asp Leu Glu
 450 455 460
 Val Leu Glu Asp Lys Asn Ala Arg Glu Phe Phe Lys Arg Val Ser Leu
 465 470 475 480
 Gly Glu Asp Leu Asn Lys Val Ile Glu Asn Phe Pro Lys Glu Leu Lys
 485 490 495
 Asp Trp Ile Phe Glu Thr Ile Glu Ser Ile Pro Pro Pro Lys Asp Pro
 500 505 510
 Glu Lys Phe Leu Gly Asp Leu Ser Glu Lys Leu Lys Ile Arg Arg Ile
 515 520 525
 Glu Arg Arg Ile Ala Glu Ile Asp Asp Met Ile Lys Lys Ala Ser Asn
 530 535 540
 Asp Glu Glu Arg Arg Leu Leu Leu Ser Met Lys Val Asp Leu Leu Arg
 545 550 555 560
 Lys Ile Lys Arg Arg
 565

<210> 155

<211> 804

<212> DNA

<213> *Thermus thermophilus*

<400> 155

atggctctac acccggtca ccctggggca ataatcgggc acgaggccgt tctcgccctc 60
 cttccccgcc tcaccgcca gacctgctc ttctccggcc ccgagggggt ggggcggcgc 120
 accgtggccc gctggtacgc ctgggggctc aaccgcggct tccccccgcc ctccctgggg 180
 gagcaccgga acgtcctcga ggtggggccc aaggcccggg acctccgggg ccgggcccag 240
 gtgcggctgg aggaggtggc gcccctcttg gagtggtgct ccagccaccc ccgggagcgg 300
 gtgaaggtgg ccatactgga ctcggccac ctctcaccg aggccgccgc caacgccctc 360
 ctcaagctcc tggaggagcc cccttctac gcccgcatcg tcctcatcgc cccaagccgc 420
 gccaccctcc tccccaccct ggcctcccgg gccacggagg tggcattcgc ccccgcgccc 480

gaggaggccc tgcgcgccct caccaggac ccggagctcc tccgctacgc cgccggggcc 540
 ccgggcccgc tccttagggc cctccaggac ccggaggggt accggggccg catggccagg 600
 gcgcaaaggg tcctgaaagc cccgcccctg gagcgctcg ctttgcttcg ggagcttttg 660
 gccgaggagg aggggggtcca cgccctccac gccgtctaa agcgcccgga gcacctcctt 720
 gccctggagc gggcgcgga ggccctggag gggtagtga gcccagagct ggtcctcgcc 780
 cggctggcct tagacttaga gaca 804

<210> 156

<211> 268

<212> PRT

<213> *Thermus thermophilus*

<400> 156

Met Ala Leu His Pro Ala His Pro Gly Ala Ile Ile Gly His Glu Ala
 1 5 10 15

Val Leu Ala Leu Leu Pro Arg Leu Thr Ala Gln Thr Leu Leu Phe Ser
 20 25 30

Gly Pro Glu Gly Val Gly Arg Arg Thr Val Ala Arg Trp Tyr Ala Trp
 35 40 45

Gly Leu Asn Arg Gly Phe Pro Pro Pro Ser Leu Gly Glu His Pro Asp
 50 55 60

Val Leu Glu Val Gly Pro Lys Ala Arg Asp Leu Arg Gly Arg Ala Glu
 65 70 75 80

Val Arg Leu Glu Glu Val Ala Pro Leu Leu Glu Trp Cys Ser Ser His
 85 90 95

Pro Arg Glu Arg Val Lys Val Ala Ile Leu Asp Ser Ala His Leu Leu
 100 105 110

Thr Glu Ala Ala Ala Asn Ala Leu Leu Lys Leu Leu Glu Glu Pro Pro
 115 120 125

Ser Tyr Ala Arg Ile Val Leu Ile Ala Pro Ser Arg Ala Thr Leu Leu
 130 135 140

Pro Thr Leu Ala Ser Arg Ala Thr Glu Val Ala Phe Ala Pro Val Pro
 145 150 155 160

Glu Glu Ala Leu Arg Ala Leu Thr Gln Asp Pro Glu Leu Leu Arg Tyr
 165 170 175

Ala Ala Gly Ala Pro Gly Arg Leu Leu Arg Ala Leu Gln Asp Pro Glu

Leu Glu Glu Ala Arg Leu Arg Gly Leu Ser Arg Phe Thr Glu Pro Thr
 20 25 30
 Pro Glu Ala Leu Ala Gln Ala Leu Ala Pro Gly Leu Phe Gly Gly Gly
 35 40 45
 Gly Ala Met Leu Asp Leu Arg Glu Val Gly Glu Ala Glu Trp Lys Ala
 50 55 60
 Leu Lys Pro Leu Leu Glu Ser Val Pro Glu Gly Val Pro Val Leu Leu
 65 70 75 80
 Leu Asp Pro Lys Pro Ser Pro Ser Arg Ala Ala Phe Tyr Arg Asn Arg
 85 90 95
 Glu Arg Arg Asp Phe Pro Thr Pro Lys Gly Lys Asp Leu Val Arg His
 100 105 110
 Leu Glu Asn Arg Ala Lys Arg Leu Gly Leu Arg Leu Pro Gly Gly Val
 115 120 125
 Ala Gln Tyr Leu Ala Ser Leu Glu Gly Asp Leu Glu Ala Leu Glu Arg
 130 135 140
 Glu Leu Glu Lys Leu Ala Leu Leu Ser Pro Pro Leu Thr Leu Glu Lys
 145 150 155 160
 Val Glu Lys Val Val Ala Leu Arg Pro Pro Leu Thr Gly Phe Asp Leu
 165 170 175
 Val Arg Ser Val Leu Glu Lys Asp Pro Lys Glu Ala Leu Leu Arg Leu
 180 185 190
 Gly Gly Leu Lys Glu Glu Gly Glu Glu Pro Leu Arg Leu Leu Gly Ala
 195 200 205
 Leu Ser Trp Gln Phe Ala Leu Leu Ala Arg Ala Phe Phe Leu Leu Arg
 210 215 220
 Glu Asn Pro Arg Pro Lys Glu Glu Asp Leu Ala Arg Leu Glu Ala His
 225 230 235 240
 Pro Tyr Ala Ala Arg Arg Ala Leu Glu Ala Ala Lys Arg Leu Thr Glu
 245 250 255
 Glu Ala Leu Lys Glu Ala Leu Asp Ala Leu Met Glu Ala Glu Lys Arg
 260 265 270

Ala Lys Gly Gly Lys Asp Pro Trp Leu Ala Leu Glu Ala Ala Val Leu
275 280 285

Arg Leu Ala Arg
290

<210> 159
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 159
gtgtgtcata tgagtaagga ttctgtccac cttcacc 37

<210> 160
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 160
gtgtgtggat ccgggggacta ctcggaagta aggg 34

<210> 161
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 161
gtgtgtcata tggaaaccac aatattccag ttccag 36

<210> 162
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 162
 gtgtgtggat ccttatccac catgagaagt atttttcac 39

<210> 163
 <211> 41
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 163
 gtgtgtcata tggaaaaagt tttttttgga aaaaactcca g 41

<210> 164
 <211> 35
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 164
 gtgtgtggat ccttaatccg cctgaacggc taacg 35

<210> 165
 <211> 41
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 165
 gtgtgtcata tgaactacgt tcccttcgcg agaaagtaca g 41

<210> 166
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 166
 gtgtgtggat ccttaaaaca gcctcgtccc gctgga 36

<210> 167
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 167
 gtgtgtcata tgcgcgttaa ggtggacagg gag 33

<210> 168
 <211> 35
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 168
 tgtgtctcga gtcattggcta caccctcatc ggcac 35

<210> 169
 <211> 47
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 169
 gtgtgtcata tgctcaataa gggtttttata ataggaagac ttacggg 47

<210> 170
 <211> 39
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 170

gtgtggatcc ttaaaaaggt atttcgtcct cttcatcgg

39

<210> 171

<211> 807

<212> DNA

<213> *Thermus thermophilus*

<400> 171

atggctcgag gcctgaaccg cgttttctctc atcggcgccc tcgccaccgg gccggacatg 60
cgctacaccc cggcgggggt cgccattttg gacctgaccc tcgccgggtca ggacctgctt 120
ctttccgata acggggggga accggaggtg tcctgggtacc accgggtgag gctcttaggc 180
cgccaggcgg agatgtgggg cgacctcttg gaccaagggc agctcgtctt cgtggagggc 240
cgcttgaggt accgccagtg ggaaagggag ggggagaagc ggagcgagct ccagatccgg 300
gccgacttcc ggacccctcg gacgaccggg ggaagaagcg ggcgaggagc agccggggcc 360
agcccaggct ccgcgcggcc ctgaaccagg tcttcctcat gggcaacctg acccggggacc 420
cggaactccg ctacaccccc cagggcaccg cggtgggccc gctgggcctg gcggtgaacg 480
agcgccgcca gggggcggag gagcgacccc acttcgtgga gggttcaggcc tggcgcgacc 540
tggcggagtg ggccgcccag ctgaggaagg gcgacggcct tttcgtgatc ggcaggttgg 600
tgaacgactc ctggaccagc tccagcggcg agcggcgctt ccagaccggt gtggaggccc 660
tcaggctgga gcgccccacc cgtggacctg cccaggcctg cccaggccgg cggaacaggt 720
cccgcgaagt ccagacgggt ggggtggaca ttgacgaagg cttggaagac tttccgccgg 780
aggaggattt gccgttttga gcacgaa 807

<210> 172

<211> 266

<212> PRT

<213> *Thermus thermophilus*

<400> 172

Met Ala Arg Gly Leu Asn Arg Val Phe Leu Ile Gly Ala Leu Ala Thr
1 5 10 15
Arg Pro Asp Met Arg Tyr Thr Pro Ala Gly Leu Ala Ile Leu Asp Leu
20 25 30
Thr Leu Ala Gly Gln Asp Leu Leu Leu Ser Asp Asn Gly Gly Glu Pro
35 40 45
Glu Val Ser Trp Tyr His Arg Val Arg Leu Leu Gly Arg Gln Ala Glu
50 55 60
Met Trp Gly Asp Leu Leu Asp Gln Gly Gln Leu Val Phe Val Glu Gly

65		70		75		80									
Arg	Leu	Glu	Tyr	Arg	Gln	Trp	Glu	Arg	Glu	Gly	Glu	Lys	Arg	Ser	Glu
				85					90					95	
Leu	Gln	Ile	Arg	Ala	Asp	Phe	Leu	Asp	Pro	Leu	Asp	Asp	Arg	Gly	Lys
			100					105					110		
Lys	Arg	Ala	Glu	Asp	Ser	Arg	Gly	Gln	Pro	Arg	Leu	Arg	Ala	Ala	Leu
		115					120					125			
Asn	Gln	Val	Phe	Leu	Met	Gly	Asn	Leu	Thr	Arg	Asp	Pro	Glu	Leu	Arg
		130					135				140				
Tyr	Thr	Pro	Gln	Gly	Thr	Ala	Val	Ala	Arg	Leu	Gly	Leu	Ala	Val	Asn
145					150					155				160	
Glu	Arg	Arg	Gln	Gly	Ala	Glu	Glu	Arg	Thr	His	Phe	Val	Glu	Val	Gln
			165						170					175	
Ala	Trp	Arg	Asp	Leu	Ala	Glu	Trp	Ala	Ala	Glu	Leu	Arg	Lys	Gly	Asp
			180					185					190		
Gly	Leu	Phe	Val	Ile	Gly	Arg	Leu	Val	Asn	Asp	Ser	Trp	Thr	Ser	Ser
		195					200					205			
Ser	Gly	Glu	Arg	Arg	Phe	Gln	Thr	Arg	Val	Glu	Ala	Leu	Arg	Leu	Glu
		210				215					220				
Arg	Pro	Thr	Arg	Gly	Pro	Ala	Gln	Ala	Cys	Pro	Gly	Arg	Arg	Asn	Arg
225					230					235				240	
Ser	Arg	Glu	Val	Gln	Thr	Gly	Gly	Val	Asp	Ile	Asp	Glu	Gly	Leu	Glu
			245						250					255	
Asp	Phe	Pro	Pro	Glu	Glu	Asp	Leu	Pro	Phe						
		260						265							

<210> 173

<211> 992

<212> DNA

<213> Bacillus stearothermophilus

<400> 173

aattccgaca tttcaattga atcgttttatt ccgcttgaaa aagaaggcaa gttgctcggt 60
gatgtgaaaa gaccggggag catcgtagct caggcgcgct ttttctctga aatcgtagaa 120
aaactgccgc aacaaacggt ggaaatcgaa acggaagaca actttttgac gatcatccgc 180

```

tcggggcact cagaattccg cctcaatggg ctaaacgccg acgaatatcc gcgcctgccg 240
caaattgaag aagaaaacgt gtttcaaate ccggctgatt tattgaaaac cgtgattcgg 300
caaacggtgt tcgccgtttc tacatcggaa acgcgcccaa tcttgacagg tgtcaactgg 360
aaagttgaac atggcgagct tgtctgcaca gcgaccgaca gtcacgcgtt agccatgcgc 420
aaagtgaata ttgagtcgga aaatgaagta tcatacaacg tcgtcatccc tggaaaaagt 480
cttaatgagc tcagcaaaat tttggatgac ggcaaccacc cggaggacat cgtcatgaca 540
gccaatcaag tgctatttaa ggccgagcac cttctcttct tttcccggt gcttgacggc 600
aactatccgg agacggcccg cttgattcca acagaaagca aaacgaccat gatcgtcaat 660
gcaaaagagt ttctgcaggc aatcgaccga gcgtccttgc ttgctcgaga aggaaggaac 720
aacgttgtga aactgacgac gcttcctgga ggaatgctcg aaatttcttc gatttctccg 780
agatcgggaa agtgacggag cagctgcaaa cggagtctct tgaaggggaa gagttgaaca 840
tttcgttcag cgcgaaatat atgatggacg cgttgccggc gcttgatgga acagacattt 900
caaatcagct tcaactggggc catgcggccg ttctgttgc gcccgcttca accgattcga 960
tgcttcagct cattttgccg gtgagaacat at 992

```

<210> 174

<211> 334

<212> PRT

<213> Bacillus stearothermophilus .

<400> 174

```

Asn Ser Asp Ile Ser Ile Ile Glu Ser Phe Ile Pro Leu Glu Lys Glu
 1             5             10             15

Gly Lys Leu Leu Val Asp Val Lys Arg Pro Gly Ser Ile Val Leu Gln
          20             25             30

Ala Arg Phe Phe Ser Glu Ile Val Lys Lys Leu Pro Gln Gln Thr Val
          35             40             45

Glu Ile Glu Thr Glu Asp Asn Phe Leu Thr Ile Ile Arg Ser Gly His
          50             55             60

Ser Glu Phe Arg Leu Asn Gly Leu Asn Ala Asp Glu Tyr Pro Arg Leu
          65             70             75             80

Pro Gln Ile Glu Glu Glu Asn Val Phe Gln Ile Pro Ala Asp Leu Leu
          85             90             95

Lys Thr Val Ile Arg Gln Thr Val Phe Ala Val Ser Thr Ser Glu Thr
          100            105            110

Arg Pro Ile Leu Thr Gly Val Asn Trp Lys Val Glu His Gly Glu Leu
          115            120            125

Val Cys Thr Ala Thr Asp Ser His Arg Leu Ala Met Arg Lys Val Lys
          130            135            140

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Ile Ile Glu Ser Glu Asn Glu Val Ser Tyr Asn Val Val Ile Pro Gly
 145 150 155 160
 Lys Ser Leu Asn Glu Leu Ser Lys Ile Ile Leu Asp Asp Gly Asn His
 165 170 175
 Pro Val Asp Ile Val Met Thr Ala Asn Gln Val Leu Phe Lys Ala Glu
 180 185 190
 His Leu Leu Phe Phe Ser Arg Leu Leu Asp Gly Asn Tyr Pro Glu Thr
 195 200 205
 Ala Arg Leu Ile Pro Thr Glu Ser Lys Thr Thr Met Ile Val Asn Ala
 210 215 220
 Lys Glu Phe Leu Gln Ala Ile Asp Arg Ala Ser Leu Leu Ala Arg Glu
 225 230 235 240
 Gly Arg Asn Asn Val Val Lys Leu Thr Thr Leu Pro Gly Gly Met Leu
 245 250 255
 Glu Ile Ser Ser Ile Ser Pro Glu Ile Gly Lys Val Thr Glu Gln Leu
 260 265 270
 Gln Thr Glu Ser Leu Glu Gly Glu Glu Leu Asn Ile Ser Phe Ser Ala
 275 280 285
 Lys Tyr Met Met Asp Ala Leu Arg Ala Leu Asp Gly Thr Asp Ile Gln
 290 295 300
 Ile Ser Phe Thr Gly Ala Met Arg Pro Phe Leu Leu Arg Pro Leu His
 305 310 315 320
 Thr Asp Ser Met Leu Gln Leu Ile Leu Pro Val Arg Thr Tyr
 325 330

<210> 175

<211> 492

<212> DNA

<213> *Bacillus stearothermophilus*

<400> 175

atgattaacc gcgtcatttt ggtcggcagg ttaacgagag atccggagtt gcgttacact 60
 ccaagcggag tggctgttgc caggtttacg ctgcgggtca accgtccgtt tacaaatcag 120
 cagggcgagc gggaaacgga ttttattcaa tgtgtcgttt ggcgccgcca ggcggaaaac 180
 gtcgccaact ttttgaaaaa ggggagcttg gctggtgtcg atggccgact gcaaaccgc 240


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agctatgaaa atcaagaagg tcggcgtgtg tacgtgacgg aagtgggtggc tgatagcgtc 300
caatttcttg agccgaaagg aacgagcagag cagcgagggg cgacagcagg cggctactat 360
ggggatccat tcccattcgg gcaagatcag aaccaccaat atccgaacga aaaaggggtt 420
ggccgcatcg atgacgatcc tttcgccaat gacggccagc cgatcgatat ttctgatgat 480
gatttgccgt tt                                     492

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<210> 176

<211> 164

<212> PRT

<213> *Bacillus stearothermophilus*

<400> 176

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Met Ile Asn Arg Val Ile Leu Val Gly Arg Leu Thr Arg Asp Pro Glu
  1             5             10             15

Leu Arg Tyr Thr Pro Ser Gly Val Ala Val Ala Thr Phe Thr Leu Ala
      20             25             30

Val Asn Arg Pro Phe Thr Asn Gln Ser Tyr Glu Asn Gln Glu Gly Arg
      35             40             45

Arg Val Tyr Val Thr Glu Val Val Ala Asp Ser Val Gln Phe Leu Glu
      50             55             60

Pro Lys Gly Thr Ser Glu Gln Arg Gly Ala Thr Ala Gly Gly Tyr Tyr
      65             70             75             80

Gln Gly Glu Arg Glu Thr Asp Phe Ile Gln Cys Val Val Trp Arg Arg
      85             90             95

Gln Ala Glu Asn Val Ala Asn Phe Leu Lys Lys Gly Ser Leu Ala Gly
      100            105            110

Val Asp Gly Arg Leu Gln Thr Arg Gly Asp Pro Phe Pro Phe Gly Gln
      115            120            125

Asp Gln Asn His Gln Tyr Pro Asn Glu Lys Gly Phe Gly Arg Ile Asp
      130            135            140

Asp Asp Pro Phe Ala Asn Asp Gly Gln Pro Ile Asp Ile Ser Asp Asp
      145            150            155            160

Asp Leu Pro Phe

```

<210> 177

<211> 1044
 <212> DNA
 <213> Bacillus stearothermophilus

<400> 177
 atgctggaac gcgtatgggg aaacattgaa aaacggcggt tttctcccct ttatttatta 60
 tacggcaatg agccgttttt attaacggaa acgtatgagc gattggtgaa cgcagcgctt 120
 ggccccgagg agcgggagtg gaacttggct gtgtacgact gcgaggaaac gccgatcgag 180
 gcggcgcttg aggaggccga gacggtgccg tttttcggcg agcggcggtgt cattctcatc 240
 aagcatccat attttttttac gtctgaaaaa gagaaggaga tcgaacatga tttggcgaag 300
 ctggaggcgt acttgaaggc gccgtcgccg ttttcgatcg tcgtcttttt cgcgccgtac 360
 gagaagcttg atgagcgaaa aaaaattacg aagctcgcca aagagcaaag cgaagtcgtc 420
 atcgccgccc cgctcgccga agcggagctg cgtgcctggg tgcggcgccg catcgagagc 480
 caaggggagc aagcaagcga cgaggcgatt gatgtcctgt tgcggcgggc cgggacgcag 540
 ctttcgcctt tggcgaatga aatcgataaa ttggccctgt ttgccggatc gggcggaacc 600
 atcgaggcgg cggcggttga gcggcttgtc gcccgcacgc cggaagaaaa cgtattttgtg 660
 cttgtcgagc aagtggcgaa gcgcgacatt ccagcagcgt tgcagacgtt ttatgatctg 720
 cttgaaaaca atgaagagcc gatcaaaatt ttggcgttgc tcgccgcca tttccgcttg 780
 ctttcgcaag tgaaatggct tgcctcctta ggctacggac aggcgcaaat tgctgcggcg 840
 ctcaaggtgc acccgttccg cgtcaagctc gctcttgctc aagcggcccg cttegtgac 900
 ggagagcttg ctgaggcgat caacgagctc gctgacgccg attacgaagt gaaaagcggg 960
 gcggtcgatc gccggttggc cgttgagctg cttctgatgc gctggggcgc ccgcccggcg 1020
 caagcggggc gccacggccg gcgg 1044

<210> 178
 <211> 348
 <212> PRT
 <213> Bacillus stearothermophilus

<400> 178
 Met Leu Glu Arg Val Trp Gly Asn Ile Glu Lys Arg Arg Phe Ser Pro
 1 5 10 15
 Leu Tyr Leu Leu Tyr Gly Asn Glu Pro Phe Leu Leu Thr Glu Thr Tyr
 20 25 30
 Glu Arg Leu Val Asn Ala Ala Leu Gly Pro Glu Glu Arg Glu Trp Asn
 35 40 45
 Leu Ala Val Tyr Asp Cys Glu Glu Thr Pro Ile Glu Ala Ala Leu Glu
 50 55 60
 Glu Ala Glu Thr Val Pro Phe Phe Gly Glu Arg Arg Val Ile Leu Ile
 65 70 75 80
 Lys His Pro Tyr Phe Phe Thr Ser Glu Lys Glu Lys Glu Ile Glu His
 85 90 95

Asp	Leu	Ala	Lys	Leu	Glu	Ala	Tyr	Leu	Lys	Ala	Pro	Ser	Pro	Phe	Ser	100	105	110	
Ile	Val	Val	Phe	Phe	Ala	Pro	Tyr	Glu	Lys	Leu	Asp	Glu	Arg	Lys	Lys	115	120	125	
Ile	Thr	Lys	Leu	Ala	Lys	Glu	Gln	Ser	Glu	Val	Val	Ile	Ala	Ala	Pro	130	135	140	
Leu	Ala	Glu	Ala	Glu	Leu	Arg	Ala	Trp	Val	Arg	Arg	Arg	Ile	Glu	Ser	145	150	155	160
Gln	Gly	Ala	Gln	Ala	Ser	Asp	Glu	Ala	Ile	Asp	Val	Leu	Leu	Arg	Arg	165	170	175	
Ala	Gly	Thr	Gln	Leu	Ser	Ala	Leu	Ala	Asn	Glu	Ile	Asp	Lys	Leu	Ala	180	185	190	
Leu	Phe	Ala	Gly	Ser	Gly	Gly	Thr	Ile	Glu	Ala	Ala	Ala	Val	Glu	Arg	195	200	205	
Leu	Val	Ala	Arg	Thr	Pro	Glu	Glu	Asn	Val	Phe	Val	Leu	Val	Glu	Gln	210	215	220	
Val	Ala	Lys	Arg	Asp	Ile	Pro	Ala	Ala	Leu	Gln	Thr	Phe	Tyr	Asp	Leu	225	230	235	240
Leu	Glu	Asn	Asn	Glu	Glu	Pro	Ile	Lys	Ile	Leu	Ala	Leu	Leu	Ala	Ala	245	250	255	
His	Phe	Arg	Leu	Leu	Ser	Gln	Val	Lys	Trp	Leu	Ala	Ser	Leu	Gly	Tyr	260	265	270	
Gly	Gln	Ala	Gln	Ile	Ala	Ala	Ala	Leu	Lys	Val	His	Pro	Phe	Arg	Val	275	280	285	
Lys	Leu	Ala	Leu	Ala	Gln	Ala	Ala	Arg	Phe	Ala	Asp	Gly	Glu	Leu	Ala	290	295	300	
Glu	Ala	Ile	Asn	Glu	Leu	Ala	Asp	Ala	Asp	Tyr	Glu	Val	Lys	Ser	Gly	305	310	315	320
Ala	Val	Asp	Arg	Arg	Leu	Ala	Val	Glu	Leu	Leu	Leu	Met	Arg	Trp	Gly	325	330	335	
Ala	Arg	Pro	Ala	Gln	Ala	Gly	Arg	His	Gly	Arg	Arg					340	345		

<210> 179
 <211> 757
 <212> DNA
 <213> *Bacillus stearothermophilus*

<400> 179
 atgcatggg aacagctagc gaaacgccag ccggtggtgg cgaaaatgct gcaaagcggc 60
 ttggaaaaag ggcggatttc tcatgcgtac ttgtttgagg ggcagcgggg gacgggcaaa 120
 aaagcggcca gtttgttggt ggcgaaacgt ttgttttgtc tgtccccaat cggagtttcc 180
 ccgtgtctag agtgccgcaa ctgccggcgc atcgactccg gcaaccaccc tgacgtccgg 240
 gtgatcggcc cagatggagg atcaatcaaa aaggaacaaa tcgaatggct gcagcaagag 300
 ttctcgaaaa cagcggtcga gtcggataaa aaaatgtaca tcgttgagca cgccgatcaa 360
 atgacgacaa gcgctgccaa cagccttctg aaatttttgg aagagccgca tccggggacg 420
 gtggcggtat tgctgactga gcaataccac cgctgctag ggacgatcgt ttcccgtgt 480
 caagtgttt cgttcgggcc gttgccggcg gcagagctcg cccagggact tgtcgaggag 540
 cacgtgccgt tgccgttggc gctgttggct gccatttga caaacagctt cgaggaagca 600
 ctggcgcttg ccaaagatag ttggtttgcc gaggcgcgaa cattagtgt acaatggtat 660
 gagatgctgg gcaagccgga gctgcagctt ttgtttttca tccacgaccg cttgtttccg 720
 cattttttgg aaagccatca gcttgacctt ggacttg 757

<210> 180
 <211> 252
 <212> PRT
 <213> *Bacillus stearothermophilus*

<400> 180
 Met Arg Trp Glu Gln Leu Ala Lys Arg Gln Pro Val Val Ala Lys Met
 1 5 10 15
 Leu Gln Ser Gly Leu Glu Lys Gly Arg Ile Ser His Ala Tyr Leu Phe
 20 25 30
 Glu Gly Gln Arg Gly Thr Gly Lys Lys Ala Ala Ser Leu Leu Leu Ala
 35 40 45
 Lys Arg Leu Phe Cys Leu Ser Pro Ile Gly Val Ser Pro Cys Leu Glu
 50 55 60
 Cys Arg Asn Cys Arg Arg Ile Asp Ser Gly Asn His Pro Asp Val Arg
 65 70 75 80
 Val Ile Gly Pro Asp Gly Gly Ser Ile Lys Lys Glu Gln Ile Glu Trp
 85 90 95
 Leu Gln Gln Glu Phe Ser Lys Thr Ala Val Glu Ser Asp Lys Lys Met

100	105	110
Tyr Ile Val Glu His Ala Asp Gln Met Thr Thr Ser Ala Ala Asn Ser		
115	120	125
Leu Leu Lys Phe Leu Glu Glu Pro His Pro Gly Thr Val Ala Val Leu		
130	135	140
Leu Thr Glu Gln Tyr His Arg Leu Leu Gly Thr Ile Val Ser Arg Cys		
145	150	155
Gln Val Leu Ser Phe Arg Pro Leu Pro Pro Ala Glu Leu Ala Gln Gly		
165	170	175
Leu Val Glu Glu His Val Pro Leu Pro Leu Ala Leu Leu Ala Ala His		
180	185	190
Leu Thr Asn Ser Phe Glu Glu Ala Leu Ala Leu Ala Lys Asp Ser Trp		
195	200	205
Phe Ala Glu Ala Arg Thr Leu Val Leu Gln Trp Tyr Glu Met Leu Gly		
210	215	220
Lys Pro Glu Leu Gln Leu Leu Phe Phe Ile His Asp Arg Leu Phe Pro		
225	230	235
His Phe Leu Glu Ser His Gln Leu Asp Leu Gly Leu		
245	250	

<210> 181
 <211> 1677
 <212> DNA
 <213> *Bacillus stearothermophilus*

<400> 181
 gtggcatacc aagcggtata tcgcgtgttt cggccgcagc gctttgcgga catggtcggc 60
 caagaacacg tgaccaagac gttgcaaagc gccctgcttc aacataaaat atcgcacgct 120
 tacttatattt cgggcccgcg cggtagacgga aaaacgagcg cagcgaaaat ttctgccaag 180
 gcggtcaact gtgaacaggc gccagcggcg gagccatgca atgagtgtcc agcttgccctc 240
 ggcatcaca atggaacggg tcccgatgtg ctggaaattg acgctgcttc caacaaccgc 300
 gtcgatgaaa ttcgtgatat ccgtgagaag gtgaaatttg cgccaacgct ggcccgcctac 360
 aaagtgtata tcatcgacga ggtgcatatg ctgtcgatcg gtgcgtttta cgcgctgttg 420
 aaaacggttg aggagccgcc gaaacacgct attttcattt tggccacgac cgagccgcac 480
 aaaattccgg cgacgatcat ttcccgctgc caacggttcg attttcgccc catcccgctt 540
 caggcgatcg tttcacggct aaagtacgct gcaagcgcgc aaggtgtcga ggcgtcagat 600
 gaggcattgt ccgccatcgc ccgtgctgca gacgggggga tgcgcgatgc gctcagcttg 660
 cttgatcaag ccatttcggt cagcgacggg aaacttcggc tcgacgacgt gctggcgatg 720

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accggggctg catcatttgc cgccttatcg agcttcatcg aagccatcca ccgcaaagat 780
acagcggcgg ttcttcagca cttggaaacg atgatggcgc aagggaaaga tccgcatcgt 840
ttggttgaag acttgatttt gtactatcgc gatttattgc tgtacaaaac cgctccctat 900
gtggaggagg cgattcaaatt tgctgtcggt gacgaagcgt tcacttcact gtcggaaatg 960
attccggttt ccaatttata cgaggccatc gagttgctga acaaaagcca gcaagagatg 1020
aagtggacaa accaccgcg ccttctgttg gaagtggcgc ttgtgaaact ttgccatcca 1080
tcagccgccg ccccgctcgt gtcggcttcc gagttggaac cgttgataaa gcggattgaa 1140
acgctggagg cggaattgcg gcgcctgaag gaacaaccgc ctgcccctcc gtcgaccgcc 1200
gcgccggtga aaaaactgtc caaaccgatg aaaacggggg gatataaagc cccggttggc 1260
cgcatttacg agctgttgaa acaggcgacg catgaagatt tagctttggt gaaaggatgc 1320
tgggcggatg tgctcgacac gttgaaacgg cagcataaag tgcgcacgc tgccttgctg 1380
caagagagcg agccggttgc agcgagcgcc tcagcgtttg tattaaaatt caaatacgaa 1440
atccactgca aaatggcgac cgatcccaca agttcgggtc aagaaaacgt cgaagcgatt 1500
ttgtttgagc tgacaaaccg ccgctttgaa atggtagcca ttccggaggg agaatgggga 1560
aaaataagag aagagttcat ccgcaataag gacgccatgg tggaaaaaag cgaagaagat 1620
ccgttaatcg ccgaagcgaa gcggctgttt ggccaagagc tgatcgaaat taaagaa 1677

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<210> 182

<211> 559

<212> PRT

<213> *Bacillus stearothermophilus*

<400> 182

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Val Ala Tyr Gln Ala Leu Tyr Arg Val Phe Arg Pro Gln Arg Phe Ala
  1               5               10               15

Asp Met Val Gly Gln Glu His Val Thr Lys Thr Leu Gln Ser Ala Leu
      20               25               30

Leu Gln His Lys Ile Ser His Ala Tyr Leu Phe Ser Gly Pro Arg Gly
      35               40               45

Thr Gly Lys Thr Ser Ala Ala Lys Ile Phe Ala Lys Ala Val Asn Cys
      50               55               60

Glu Gln Ala Pro Ala Ala Glu Pro Cys Asn Glu Cys Pro Ala Cys Leu
      65               70               75               80

Gly Ile Thr Asn Gly Thr Val Pro Asp Val Leu Glu Ile Asp Ala Ala
      85               90               95

Ser Asn Asn Arg Val Asp Glu Ile Arg Asp Ile Arg Glu Lys Val Lys
      100              105              110

Phe Ala Pro Thr Ser Ala Arg Tyr Lys Val Tyr Ile Ile Asp Glu Val
      115              120              125

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His	Met	Leu	Ser	Ile	Gly	Ala	Phe	Asn	Ala	Leu	Leu	Lys	Thr	Leu	Glu	130	135	140	
Glu	Pro	Pro	Lys	His	Val	Ile	Phe	Ile	Leu	Ala	Thr	Thr	Glu	Pro	His	145	150	155	160
Lys	Ile	Pro	Ala	Thr	Ile	Ile	Ser	Arg	Cys	Gln	Arg	Phe	Asp	Phe	Arg	165	170	175	
Arg	Ile	Pro	Leu	Gln	Ala	Ile	Val	Ser	Arg	Leu	Lys	Tyr	Val	Ala	Ser	180	185	190	
Ala	Gln	Gly	Val	Glu	Ala	Ser	Asp	Glu	Ala	Leu	Ser	Ala	Ile	Ala	Arg	195	200	205	
Ala	Ala	Asp	Gly	Gly	Met	Arg	Asp	Ala	Leu	Ser	Leu	Leu	Asp	Gln	Ala	210	215	220	
Ile	Ser	Phe	Ser	Asp	Gly	Lys	Leu	Arg	Leu	Asp	Asp	Val	Leu	Ala	Met	225	230	235	240
Thr	Gly	Ala	Ala	Ser	Phe	Ala	Ala	Leu	Ser	Ser	Phe	Ile	Glu	Ala	Ile	245	250	255	
His	Arg	Lys	Asp	Thr	Ala	Ala	Val	Leu	Gln	His	Leu	Glu	Thr	Met	Met	260	265	270	
Ala	Gln	Gly	Lys	Asp	Pro	His	Arg	Leu	Val	Glu	Asp	Leu	Ile	Leu	Tyr	275	280	285	
Tyr	Arg	Asp	Leu	Leu	Leu	Tyr	Lys	Thr	Ala	Pro	Tyr	Val	Glu	Gly	Ala	290	295	300	
Ile	Gln	Ile	Ala	Val	Val	Asp	Glu	Ala	Phe	Thr	Ser	Leu	Ser	Glu	Met	305	310	315	320
Ile	Pro	Val	Ser	Asn	Leu	Tyr	Glu	Ala	Ile	Glu	Leu	Leu	Asn	Lys	Ser	325	330	335	
Gln	Gln	Glu	Met	Lys	Trp	Thr	Asn	His	Pro	Arg	Leu	Leu	Leu	Glu	Val	340	345	350	
Ala	Leu	Val	Lys	Leu	Cys	His	Pro	Ser	Ala	Ala	Ala	Pro	Ser	Leu	Ser	355	360	365	
Ala	Ser	Glu	Leu	Glu	Pro	Leu	Ile	Lys	Arg	Ile	Glu	Thr	Leu	Glu	Ala	370	375	380	

Glu Leu Arg Arg Leu Lys Glu Gln Pro Pro Ala Pro Pro Ser Thr Ala
 385 390 395 400
 Ala Pro Val Lys Lys Leu Ser Lys Pro Met Lys Thr Gly Gly Tyr Lys
 405 410 415
 Ala Pro Val Gly Arg Ile Tyr Glu Leu Leu Lys Gln Ala Thr His Glu
 420 425 430
 Asp Leu Ala Leu Val Lys Gly Cys Trp Ala Asp Val Leu Asp Thr Leu
 435 440 445
 Lys Arg Gln His Lys Val Ser His Ala Ala Leu Leu Gln Glu Ser Glu
 450 455 460
 Pro Val Ala Ala Ser Ala Ser Ala Phe Val Leu Lys Phe Lys Tyr Glu
 465 470 475 480
 Ile His Cys Lys Met Ala Thr Asp Pro Thr Ser Ser Val Lys Glu Asn
 485 490 495
 Val Glu Ala Ile Leu Phe Glu Leu Thr Asn Arg Arg Phe Glu Met Val
 500 505 510
 Ala Ile Pro Glu Gly Glu Trp Gly Lys Ile Arg Glu Glu Phe Ile Arg
 515 520 525
 Asn Lys Asp Ala Met Val Glu Lys Ser Glu Glu Asp Pro Leu Ile Ala
 530 535 540
 Glu Ala Lys Arg Leu Phe Gly Glu Glu Leu Ile Glu Ile Lys Glu
 545 550 555

<210> 183

<211> 4301

<212> DNA

<213> *Bacillus stearothermophilus*

<400> 183

atggtgacaa aagagcaaaa agagcggttt ctcacacctgc ttgagcagct gaagatgacg 60
 tcggacgaat ggatgccgca ttttcgtgag gcagccattc gcaaagtcgt gatcgataaa 120
 gaggagaaaa gctggcattt ttattttcag ttcgacaacg tgctgccggt tcatgtatac 180
 aaaacgtttg ccgatcggct gcagacggcg ttccgccata tcgccgccgt ccgccatacg 240
 atggaggtcg aagcgccgcg cgtaactgag gcggtatgtc aggcgtattg gccgctttgc 300
 cttgccgagc tgcaagaagg catgtcgccg cttgtcgatt ggctcagccg gcagacgcct 360
 gagctgaaag gaaacaagct gcttgctggt gcccgccatg aagcggaagc gctggcgatc 420
 aaacggcggc tcgccaaaaa aatcgctgat gtgtacgctt cgtttggtt tccccccctt 480

cagcttgacg	tcagcgtcga	gccgtccaag	caagaaatgg	aacagttttt	ggcgcaaaaa	540
cagcaagagg	acgaagagcg	agcgcttgct	gtactgaccg	atttagcgag	ggaagaagaa	600
aaggccgcgt	ctgcgcgcgc	gtccgggtccg	cttgtcatcg	gctatccgat	ccgcgacgag	660
gagccggtgc	ggcggttgga	aacgatcgtc	gaagaagagc	ggcgcgtcgt	tgtgcaaggc	720
tatgtatttg	acgccgaagt	gagcgaatta	aaaagcggcc	gcacgctgtt	gaccatgaaa	780
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gagcttatga	gcggcgctcaa	aaaaggcatg	tgggtgaaag	tgcgcggcag	cgtgcaaaac	900
gatacgttcg	tccgtgattt	ggatcatcatc	gccaacgatt	tgaacgaaat	cgccgcaaac	960
gaacggcaag	atacggcgcc	ggaaggggaa	aagagggtcg	agctccattt	gcataccccg	1020
atgagccaaa	tggacgcggt	cacctcggtg	acaaaactca	ttgagcaagc	gaaaaaatgg	1080
gggcatccgg	cgatcgccgt	caccgaccat	gccgttggtc	agtcgtttcc	ggaggcctac	1140
agcgcggcga	aaaaacacgg	catgaagggtc	atttacggcc	ttgaggcgaa	catcgtcgac	1200
gatggcggtc	cgatcgccct	caatgagacg	caccgcccgtc	tttcggagga	aacgtacgtc	1260
gtctttgacg	tcgagacgac	gggcctgtcg	gctgtgtaca	atacgatcat	tgagctggcg	1320
gcgggtgaaag	tgaagacgag	cgagatcatc	gaccgattca	tgtcgtttgc	caaccctgga	1380
catccgttgt	cgggtgacaac	gatggagctg	actgggatca	ccgatgagat	ggtgaaagac	1440
gccccgaagc	cggacgaggt	gctagcccgt	tttggtgact	gggcccgcga	tgcgacgctt	1500
gttgcccaca	acgccagctt	tgacatcggt	tttttaaacy	cgggcctcgc	tcgcatgggg	1560
cgcggaacaa	tcgcgaatcc	agtcatcgat	acgctcgagc	tggcccgttt	tttatacccc	1620
gatttgaaaa	accatcggtc	caatacattg	tgcaaaaaat	ttgacattga	attgacgcag	1680
catcaccgcg	ccatctacga	cgcgagggcg	accgggcatt	tgtttatgcg	gctgttgaa	1740
gaagcggaag	agcgcgcat	actgtttcat	gacgaattaa	acagccgcac	gcacagcgaa	1800
gcgtcctatc	ggcttgcgcg	cccgttccat	gtgacgctgt	tggcgcaaaa	cgagactgga	1860
ttgaaaaatt	tgttcaagct	tgtgtcattg	tcgcacattc	aatattttca	ccgtgtgccg	1920
cgcatcccgc	gctccgtgct	cgtcaagcac	cgcgacggcc	tgcttgctcg	ctcggtgtgc	1980
gacaaaggag	agctgtttga	caacttgatc	caaaaggcgc	cggaagaagt	cgaagacatc	2040
gcccgttttt	acgattttct	tgaagtgcac	ccgcgggacg	tgtacaagcc	gctcatcgag	2100
atggattatg	tgaagacga	agagatgatc	aaaaacatca	tccgcagcat	cgtcgccctt	2160
ggtgagaagc	ttgacatccc	ggttgctgcc	actggcaacg	tccattactt	gaaccagaa	2220
gataaaattt	accgaaaaat	cttaatccat	tcgcaaggcg	gggcgaatcc	gctcaaccgc	2280
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atcggcgatg	tcaagccgat	caaagatgag	ctgtatacgc	cgcgcatgga	aggggcggac	2460
gaggaaatca	gggaaatgag	ctaccggcgg	gcgaaggaaa	tttacggcga	cccgttgccg	2520
aaacttggtg	aagagcggct	tgagaaggag	ctaaaaagca	tcacgcggca	tggctttgcc	2580
gtcatttatt	tgatctcgca	caagcttggtg	aaaaaatcgc	tcgatgacgg	ctacctgtgc	2640
gggtcgcgcg	gatcggtcgg	ctcgctcgttt	gtcgcgacga	tgacggaaat	caccgagggtc	2700
aatccgctgc	cgccgcatta	cgtttgcccc	aactgcaagc	attcgaggtt	ctttaacgac	2760
ggttcagtcg	gctcagggtt	tgatttgccg	gataaaaact	gcccgcgatg	tgggacgaaa	2820
tacaagaaag	acgggcacga	catcccgttt	gagacgtttc	tcggctttta	aggcgacaaa	2880
gtgccggata	tcgacttgaa	cttttcgggc	gaataccagc	cgcgcgccca	caactatacg	2940
aaagtgtgtg	ttggcgaaga	caacgtctac	cgcgccggga	cgattggcac	ggtcgctgac	3000
aaaacggcgt	acggatttgt	caaagcgtat	gcgagcgacc	ataacttaga	gctgcgcggc	3060
gcggaaatcg	acggctcgcg	gctggctgca	ccgggggtgaa	gcggacgacc	gggcagcatc	3120
cgggcgccat	catcgctcgtc	ccggattata	tggaaattta	cgatttttacg	ccgattcaat	3180
atccggccga	tgacacgtcc	tctgaatggc	ggacgaccca	tttcgacttc	cattcgatcc	3240
acgacaattt	gttgaagctc	gatattctcg	ggcacgacga	tccgacggtc	attcgcatgc	3300
tgcaagattt	aagcggcatc	gatccgaaaa	cgatcccgcg	cgacgaccgc	gatgtgatgg	3360

```

gcatttttcag cagcaccgag ccgcttggcg ttacgccgga gcaaatacatg tgcaatgtcg 3420
gcacgatcgg cattccggag tttggcacgc gcttcgttcg gcaaattgtg gaagagacaa 3480
ggccaaaaaac gttttccgaa ctctgtgcaaa tttccggctt gtcgcacggc accgatgtgt 3540
ggctcggcaa cgcgcaagag ctcatccaac acggcacgtg tacgttatcg gaagtcacgtg 3600
gctgccgcga cgacattatg gtctatttga tttaccgcgg gctcgagccg tcgctcgctt 3660
ttaaaatcat ggaatccgtg cgcaaaggaa aaggcttaac gccggagttt gaagcagaaa 3720
tgcgcaaaaca tgacgtgccg gagtgggtaca tcgattcatg caaaaaaatc aagtacatgt 3780
tcccgaagc gcacgccgcc gcttacgtgt taatggcggg gcgcacgcc tactttaagg 3840
tgacccatcc gcttttgtat tacgcgtcgt actttacggg gcgggcggag gactttgacc 3900
ttgacgccat gatcaaagga tcacccgccca ttcgcaagcg gattgaggaa atcaacgccca 3960
aaggcattca ggcgacggcg aaagaaaaaa gcttgctcac ggttcttgag gtggccttag 4020
agatgtgcga gcgcggcttt tccttttaaaa atatcgattt gtaccgctcg caggcgacgg 4080
aattcgatcat tgacggcaat tctctcattc cgccgttcaa cgccattccg gggcttggga 4140
cgaacgtggc gcaggcgatc gtgcgcgccc gcgaggaagg cgagtttttg tcgaaggagg 4200
atgtgcaaca gcgcggcaaa ttgtcgaaaa cgctgctcga gtatctagaa agccgcgggt 4260
gccttgactc gcttcagac cataaccagc tgcgctgtt t 4301

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<210> 184

<211> 1433

<212> PRT

<213> *Bacillus stearothermophilus*

<400> 184

```

Met Val Thr Lys Glu Gln Lys Glu Arg Phe Leu Ile Leu Leu Glu Gln
  1              5              10              15

```

```

Leu Lys Met Thr Ser Asp Glu Trp Met Pro His Phe Arg Glu Ala Ala
      20              25              30

```

```

Ile Arg Lys Val Val Ile Asp Lys Glu Glu Lys Ser Trp His Phe Tyr
      35              40              45

```

```

Phe Gln Phe Asp Asn Val Leu Pro Val His Val Tyr Lys Thr Phe Ala
      50              55              60

```

```

Asp Arg Leu Gln Thr Ala Phe Arg His Ile Ala Ala Val Arg His Thr
      65              70              75              80

```

```

Met Glu Val Glu Ala Pro Arg Val Thr Glu Ala Asp Val Gln Ala Tyr
      85              90              95

```

```

Trp Pro Leu Cys Leu Ala Glu Leu Gln Glu Gly Met Ser Pro Leu Val
      100             105             110

```

```

Asp Trp Leu Ser Arg Gln Thr Pro Glu Leu Lys Gly Asn Lys Leu Leu
      115             120             125

```

Val	Val	Ala	Arg	His	Glu	Ala	Glu	Ala	Leu	Ala	Ile	Lys	Arg	Arg	Phe	130	135	140	
Ala	Lys	Lys	Ile	Ala	Asp	Val	Tyr	Ala	Ser	Phe	Gly	Phe	Pro	Pro	Leu	145	150	155	160
Gln	Leu	Asp	Val	Ser	Val	Glu	Pro	Ser	Lys	Gln	Glu	Met	Glu	Gln	Phe	165	170	175	
Leu	Ala	Gln	Lys	Gln	Gln	Glu	Asp	Glu	Glu	Arg	Ala	Leu	Ala	Val	Leu	180	185	190	
Thr	Asp	Leu	Ala	Arg	Glu	Glu	Glu	Lys	Ala	Ala	Ser	Ala	Pro	Pro	Ser	195	200	205	
Gly	Pro	Leu	Val	Ile	Gly	Tyr	Pro	Ile	Arg	Asp	Glu	Glu	Pro	Val	Arg	210	215	220	
Arg	Leu	Glu	Thr	Ile	Val	Glu	Glu	Glu	Arg	Arg	Val	Val	Val	Gln	Gly	225	230	235	240
Tyr	Val	Phe	Asp	Ala	Glu	Val	Ser	Glu	Leu	Lys	Ser	Gly	Arg	Thr	Leu	245	250	255	
Leu	Thr	Met	Lys	Ile	Thr	Asp	Tyr	Thr	Asn	Ser	Ile	Leu	Val	Lys	Met	260	265	270	
Phe	Ser	Arg	Asp	Lys	Glu	Asp	Ala	Glu	Leu	Met	Ser	Gly	Val	Lys	Lys	275	280	285	
Gly	Met	Trp	Val	Lys	Val	Arg	Gly	Ser	Val	Gln	Asn	Asp	Thr	Phe	Val	290	295	300	
Arg	Asp	Leu	Val	Ile	Ile	Ala	Asn	Asp	Leu	Asn	Glu	Ile	Ala	Ala	Asn	305	310	315	320
Glu	Arg	Gln	Asp	Thr	Ala	Pro	Glu	Gly	Glu	Lys	Arg	Val	Glu	Leu	His	325	330	335	
Leu	His	Thr	Pro	Met	Ser	Gln	Met	Asp	Ala	Val	Thr	Ser	Val	Thr	Lys	340	345	350	
Leu	Ile	Glu	Gln	Ala	Lys	Lys	Trp	Gly	His	Pro	Ala	Ile	Ala	Val	Thr	355	360	365	
Asp	His	Ala	Val	Val	Gln	Ser	Phe	Pro	Glu	Ala	Tyr	Ser	Ala	Ala	Lys	370	375	380	

Lys His Gly Met Lys Val Ile Tyr Gly Leu Glu Ala Asn Ile Val Asp
 385 390 395 400
 Asp Gly Val Pro Ile Ala Tyr Asn Glu Thr His Arg Arg Leu Ser Glu
 405 410 415
 Glu Thr Tyr Val Val Phe Asp Val Glu Thr Thr Gly Leu Ser Ala Val
 420 425 430
 Tyr Asn Thr Ile Ile Glu Leu Ala Ala Val Lys Val Lys Asp Gly Glu
 435 440 445
 Ile Ile Asp Arg Phe Met Ser Phe Ala Asn Pro Gly His Pro Leu Ser
 450 455 460
 Val Thr Thr Met Glu Leu Thr Gly Ile Thr Asp Glu Met Val Lys Asp
 465 470 475 480
 Ala Pro Lys Pro Asp Glu Val Leu Ala Arg Phe Val Asp Trp Ala Gly
 485 490 495
 Asp Ala Thr Leu Val Ala His Asn Ala Ser Phe Asp Ile Gly Phe Leu
 500 505 510
 Asn Ala Gly Leu Ala Arg Met Gly Arg Gly Lys Ile Ala Asn Pro Val
 515 520 525
 Ile Asp Thr Leu Glu Leu Ala Arg Phe Leu Tyr Pro Asp Leu Lys Asn
 530 535 540
 His Arg Leu Asn Thr Leu Cys Lys Lys Phe Asp Ile Glu Leu Thr Gln
 545 550 555 560
 His His Arg Ala Ile Tyr Asp Ala Glu Ala Thr Gly His Leu Leu Met
 565 570 575
 Arg Leu Leu Lys Glu Ala Glu Glu Arg Gly Ile Leu Phe His Asp Glu
 580 585 590
 Leu Asn Ser Arg Thr His Ser Glu Ala Ser Tyr Arg Leu Ala Arg Pro
 595 600 605
 Phe His Val Thr Leu Leu Ala Gln Asn Glu Thr Gly Leu Lys Asn Leu
 610 615 620
 Phe Lys Leu Val Ser Leu Ser His Ile Gln Tyr Phe His Arg Val Pro
 625 630 635 640

Arg	Ile	Pro	Arg	Ser	Val	Leu	Val	Lys	His	Arg	Asp	Gly	Leu	Leu	Val	645	650	655
Gly	Ser	Gly	Cys	Asp	Lys	Gly	Glu	Leu	Phe	Asp	Asn	Leu	Ile	Gln	Lys	660	665	670
Ala	Pro	Glu	Glu	Val	Glu	Asp	Ile	Ala	Arg	Phe	Tyr	Asp	Phe	Leu	Glu	675	680	685
Val	His	Pro	Pro	Asp	Val	Tyr	Lys	Pro	Leu	Ile	Glu	Met	Asp	Tyr	Val	690	695	700
Lys	Asp	Glu	Glu	Met	Ile	Lys	Asn	Ile	Ile	Arg	Ser	Ile	Val	Ala	Leu	705	710	715
Gly	Glu	Lys	Leu	Asp	Ile	Pro	Val	Val	Ala	Thr	Gly	Asn	Val	His	Tyr	725	730	735
Leu	Asn	Pro	Glu	Asp	Lys	Ile	Tyr	Arg	Lys	Ile	Leu	Ile	His	Ser	Gln	740	745	750
Gly	Gly	Ala	Asn	Pro	Leu	Asn	Arg	His	Glu	Leu	Pro	Asp	Val	Tyr	Phe	755	760	765
Arg	Thr	Thr	Asn	Glu	Met	Leu	Asp	Cys	Phe	Ser	Phe	Leu	Gly	Pro	Glu	770	775	780
Lys	Ala	Lys	Glu	Ile	Val	Val	Asp	Asn	Thr	Gln	Lys	Ile	Ala	Ser	Leu	785	790	795
Ile	Gly	Asp	Val	Lys	Pro	Ile	Lys	Asp	Glu	Leu	Tyr	Thr	Pro	Arg	Ile	805	810	815
Glu	Gly	Ala	Asp	Glu	Glu	Ile	Arg	Glu	Met	Ser	Tyr	Arg	Arg	Ala	Lys	820	825	830
Glu	Ile	Tyr	Gly	Asp	Pro	Leu	Pro	Lys	Leu	Val	Glu	Glu	Arg	Leu	Glu	835	840	845
Lys	Glu	Leu	Lys	Ser	Ile	Ile	Gly	His	Gly	Phe	Ala	Val	Ile	Tyr	Leu	850	855	860
Ile	Ser	His	Lys	Leu	Val	Lys	Lys	Ser	Leu	Asp	Asp	Gly	Tyr	Leu	Val	865	870	875
Gly	Ser	Arg	Gly	Ser	Val	Gly	Ser	Ser	Phe	Val	Ala	Thr	Met	Thr	Glu	885	890	895

Ile Thr Glu Val Asn Pro Leu Pro Pro His Tyr Val Cys Pro Asn Cys	900	905	910
Lys His Ser Glu Phe Phe Asn Asp Gly Ser Val Gly Ser Gly Phe Asp	915	920	925
Leu Pro Asp Lys Asn Cys Pro Arg Cys Gly Thr Lys Tyr Lys Lys Asp	930	935	940
Gly His Asp Ile Pro Phe Glu Thr Phe Leu Gly Phe Lys Gly Asp Lys	945	950	955
Val Pro Asp Ile Asp Leu Asn Phe Ser Gly Glu Tyr Gln Pro Arg Ala	965	970	975
His Asn Tyr Thr Lys Val Leu Phe Gly Glu Asp Asn Val Tyr Arg Ala	980	985	990
Gly Thr Ile Gly Thr Val Ala Asp Lys Thr Ala Tyr Gly Phe Val Lys	995	1000	1005
Ala Tyr Ala Ser Asp His Asn Leu Glu Leu Arg Gly Ala Glu Ile Asp	1010	1015	1020
Leu Ala Ala Gly Cys Thr Gly Val Lys Arg Thr Thr Gly Gln His Pro	1025	1030	1035
Gly Gly Ile Ile Val Val Pro Asp Tyr Met Glu Ile Tyr Asp Phe Thr	1045	1050	1055
Pro Ile Gln Tyr Pro Ala Asp Asp Thr Ser Ser Glu Trp Arg Thr Thr	1060	1065	1070
His Phe Asp Phe His Ser Ile His Asp Asn Leu Leu Lys Leu Asp Ile	1075	1080	1085
Leu Gly His Asp Asp Pro Thr Val Ile Arg Met Leu Gln Asp Leu Ser	1090	1095	1100
Gly Ile Asp Pro Lys Thr Ile Pro Thr Asp Asp Pro Asp Val Met Gly	1105	1110	1115
Ile Phe Ser Ser Thr Glu Pro Leu Gly Val Thr Pro Glu Gln Ile Met	1125	1130	1135
Cys Asn Val Gly Thr Ile Gly Ile Pro Glu Phe Gly Thr Arg Phe Val	1140	1145	1150

Arg Gln Met Leu Glu Glu Thr Arg Pro Lys Thr Phe Ser Glu Leu Val
 1155 1160 1165

Gln Ile Ser Gly Leu Ser His Gly Thr Asp Val Trp Leu Gly Asn Ala
 1170 1175 1180

Gln Glu Leu Ile Gln Asn Gly Thr Cys Thr Leu Ser Glu Val Ile Gly
 1185 1190 1195 1200

Cys Arg Asp Asp Ile Met Val Tyr Leu Ile Tyr Arg Gly Leu Glu Pro
 1205 1210 1215

Ser Leu Ala Phe Lys Ile Met Glu Ser Val Arg Lys Gly Lys Gly Leu
 1220 1225 1230

Thr Pro Glu Phe Glu Ala Glu Met Arg Lys His Asp Val Pro Glu Trp
 1235 1240 1245

Tyr Ile Asp Ser Cys Lys Lys Ile Lys Tyr Met Phe Pro Lys Ala His
 1250 1255 1260

Ala Ala Ala Tyr Val Leu Met Ala Val Arg Ile Ala Tyr Phe Lys Val
 1265 1270 1275 1280

His His Pro Leu Leu Tyr Tyr Ala Ser Tyr Phe Thr Val Arg Ala Glu
 1285 1290 1295

Asp Phe Asp Leu Asp Ala Met Ile Lys Gly Ser Pro Ala Ile Arg Lys
 1300 1305 1310

Arg Ile Glu Glu Ile Asn Ala Lys Gly Ile Gln Ala Thr Ala Lys Glu
 1315 1320 1325

Lys Ser Leu Leu Thr Val Leu Glu Val Ala Leu Glu Met Cys Glu Arg
 1330 1335 1340

Gly Phe Ser Phe Lys Asn Ile Asp Leu Tyr Arg Ser Gln Ala Thr Glu
 1345 1350 1355 1360

Phe Val Ile Asp Gly Asn Ser Leu Ile Pro Pro Phe Asn Ala Ile Pro
 1365 1370 1375

Gly Leu Gly Thr Asn Val Ala Gln Ala Ile Val Arg Ala Arg Glu Glu
 1380 1385 1390

Gly Glu Phe Leu Ser Lys Glu Asp Leu Gln Gln Arg Gly Lys Leu Ser
 1395 1400 1405

Lys Thr Leu Leu Glu Tyr Leu Glu Ser Arg Gly Cys Leu Asp Ser Leu
 1410 1415 1420

Pro Asp His Asn Gln Leu Ser Leu Phe
 1425 1430

<210> 185

<211> 199

<212> PRT

<213> Thermus thermophilus

<400> 185

Thr Pro Lys Gly Lys Asp Leu Val Arg His Leu Glu Asn Arg Ala Lys
 1 5 10 15

Arg Leu Gly Leu Arg Leu Pro Gly Gly Val Ala Gln Tyr Leu Ala Ser
 20 25 30

Leu Glu Gly Asp Leu Glu Ala Leu Glu Arg Glu Leu Glu Lys Leu Ala
 35 40 45

Leu Leu Ser Pro Pro Leu Thr Leu Glu Lys Val Glu Lys Val Val Ala
 50 55 60

Leu Arg Pro Pro Leu Thr Gly Phe Asp Leu Val Arg Ser Val Leu Glu
 65 70 75 80

Lys Asp Pro Lys Glu Ala Leu Leu Arg Leu Gly Arg Leu Lys Glu Glu
 85 90 95

Gly Glu Glu Pro Leu Arg Leu Leu Gly Ala Leu Ser Trp Gln Phe Ala
 100 105 110

Leu Leu Ala Arg Ala Phe Phe Leu Leu Arg Glu Met Pro Arg Pro Lys
 115 120 125

Glu Glu Asp Leu Ala Arg Leu Glu Ala His Pro Tyr Ala Ala Lys Lys
 130 135 140

Ala Leu Leu Glu Ala Ala Arg Arg Leu Thr Glu Glu Ala Leu Lys Glu
 145 150 155 160

Ala Leu Asp Ala Leu Met Glu Ala Glu Lys Arg Ala Lys Gly Gly Lys
 165 170 175

Asp Pro Trp Leu Ala Leu Glu Ala Ala Val Leu Arg Leu Ala Arg Pro
 180 185 190

Ala Gly Gln Pro Arg Val Asp
195

<210> 186
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<400> 186
gcccgatacc tcgcctccct cgagggg 27

<210> 187
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<400> 187
ggcccccttg gccttctcgg cctccat 27

<210> 188
<211> 331
<212> DNA
<213> *Thermus thermophilus*

<400> 188
agactcgagg ccctggagcg ggagctggag aagcttgccc tcctctcccc acccctcacc 60
ctggagaagg tggagaaggt ggtggccctg aggccccccc tcacgggctt tgacctggtg 120
cgctccgtcc tggagaagga cccaaggag gccctcctgc gcctcaggcg cctcaggag 180
gagggggagg agccctcag gctcctcggg gccctctcct ggcagttcgc cctcctcgcc 240
cgggccttct tcctcctccg ggaaaacccc aggccaagg aggaggacct cgcccgccctc 300
gaggcccacc cctacgccgc caagaaggcc a 331

<210> 189
<211> 110
<212> PRT
<213> *Thermus thermophilus*

<400> 189

Arg Leu Glu Ala Leu Glu Arg Glu Leu Glu Lys Leu Ala Leu Leu Ser
1 5 10 15

Pro Pro Leu Thr Leu Glu Lys Val Glu Lys Val Val Ala Leu Arg Pro
20 25 30

Pro Leu Thr Gly Phe Asp Leu Val Arg Ser Val Leu Glu Lys Asp Pro
35 40 45

Lys Glu Ala Leu Leu Arg Leu Arg Arg Leu Arg Glu Glu Gly Glu Glu
50 55 60

Pro Leu Arg Leu Leu Gly Ala Leu Ser Trp Gln Phe Ala Leu Leu Ala
65 70 75 80

Arg Ala Phe Phe Leu Leu Arg Glu Asn Pro Arg Pro Lys Glu Glu Asp
85 90 95

Leu Ala Arg Leu Glu Ala His Pro Tyr Ala Ala Lys Lys Ala
100 105 110

<210> 190

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 190

gtggtgtcta gacatcataa cggttctggc a 31

<210> 191

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR Primer

<400> 191

gagggccacc accttctcca ccttctc 27

<210> 192

<211> 25
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR Primer

<400> 192
ctccgtcctg gagaaggacc ccaag

25

<210> 193
<211> 29
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<220>
<221> primer_bind
<222> (15)
<223> S at position 15 can be either C or G

<220>
<221> primer_bind
<222> (27)
<223> S at position 27 can be either C or G

<400> 193
cgcgattca acgcsctcct caagacsct

29

<210> 194
<211> 31
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 194
gacacttaac atatggtcat cgccttcacc g

31

<210> 195
<211> 38
<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 195

gtgtgtgaat tcgggtcaac gggcgaggcg gaggaccg

38

<210> 196

<211> 10

<212> PRT

<213> *Deinococcus radiodurans*

<400> 196

Val Ile Leu Asn Pro Gly Ser Val Gly Gln

1 5 10

<210> 197

<211> 10

<212> PRT

<213> *Methanococcus jannaschii*

<400> 197

Tyr Leu Ile Asn Pro Gly Ser Val Gly Gln

1 5 10

<210> 198

<211> 10

<212> PRT

<213> *Thermotoga maritima*

<400> 198

Leu Val Leu Asn Pro Gly Ser Ala Gly Arg

1 5 10

<210> 199

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 199

ctggtgaacc cgggctccgt gggccagc

28

<210> 200

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: polypeptide

<400> 200

Leu Leu Val Asn Pro Gly Ser Val Gly Gln

1

5

10

<210> 201

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 201

ctcgaggagc ttgaggaggg tggtggc

27

<210> 202

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: polypeptide

<400> 202

Ala Asn Thr Leu Leu Lys Leu Leu Glu

1

5

<210> 203

<211> 32

<212> PRT

<213> Deinococcus radiodurans

<400> 203

Gly Phe Gly Gly Val Gln Leu His Ala Ala His Gly Tyr Leu Leu Ser

1	5	10	15
Gln Phe Leu Ser Pro Arg His Asn Val Arg Glu Asp Glu Tyr Gly Gly			
20	25	30	

<210> 204
 <211> 32
 <212> PRT
 <213> *Caenorhabditis elegans*

<400> 204
Gly Phe Asp Gly Ile Gln Leu His Gly Ala His Gly Tyr Leu Leu Ser
1 5 10 15
Gln Phe Thr Ser Pro Thr Thr Asn Lys Arg Val Asp Lys Tyr Gly Gly
20 25 30

<210> 205
 <211> 32
 <212> PRT
 <213> *Pseudomonas aeruginosa*

<400> 205
Gly Phe Ser Gly Val Glu Ile His Ala Ala His Gly Tyr Leu Leu Ser
1 5 10 15
Gln Phe Leu Ser Pro Leu Ser Asn Arg Arg Ser Asp Ala Trp Gly Gly
20 25 30

<210> 206
 <211> 32
 <212> PRT
 <213> *Archaeoglobus fulgidus*

<400> 206
Gly Phe Asp Ala Val Gln Leu His Ala Ala His Gly Tyr Leu Leu Ser

1 5 10 15

Glu Phe Ile Ser Pro His Val Asn Arg Arg Lys Asp Glu Tyr Gly Gly
20 25 30

<210> 207

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 207

catcctggac tcggcccacc tcctcaccga

30

<210> 208

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: polypeptide

<400> 208

Ile Leu Asp Ser Ala His Leu Leu Thr

1

5

<210> 209

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 209

gaggaggtag ccgtggggccg cgtggagctc cac

33

<210> 210

<211> 11

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: polypeptide

<400> 210
Val Glu Leu His Ala Ala His Gly Tyr Leu Leu
1 5 10

<210> 211
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<400> 211
ggctttccca tatggctcta caccggctc ac

32

<210> 212
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<400> 212
gcgtgatcc acggtcatgt ctctaagtc

29